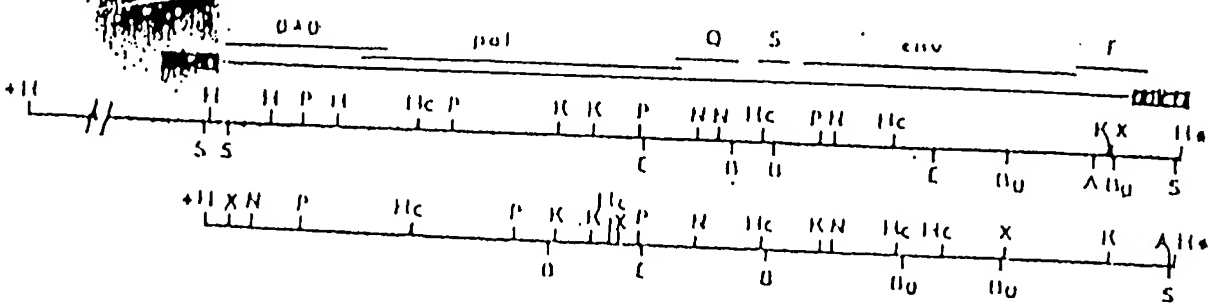

gag
pol
Q
S
env
F
LAV eli
LAV mal

FIG. 1A

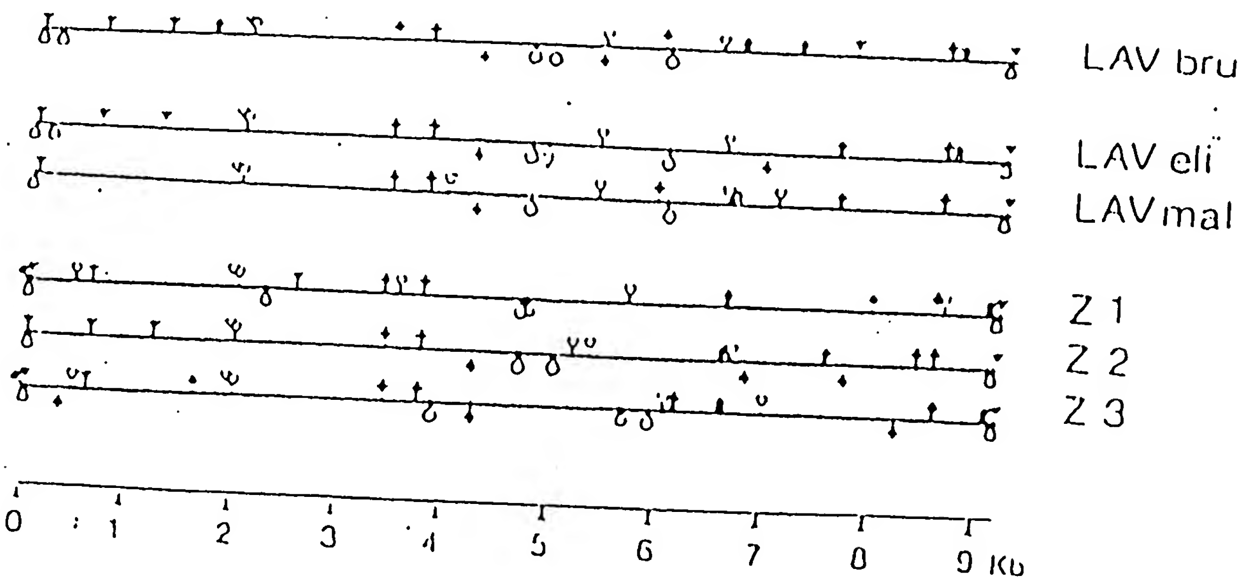

LAV bru
LAV eli
LAV mal
Z 1
Z 2
Z 3
0
1
2
3
4
5
6
7
8
9 Kb

FIG. 1B

FIG. 2

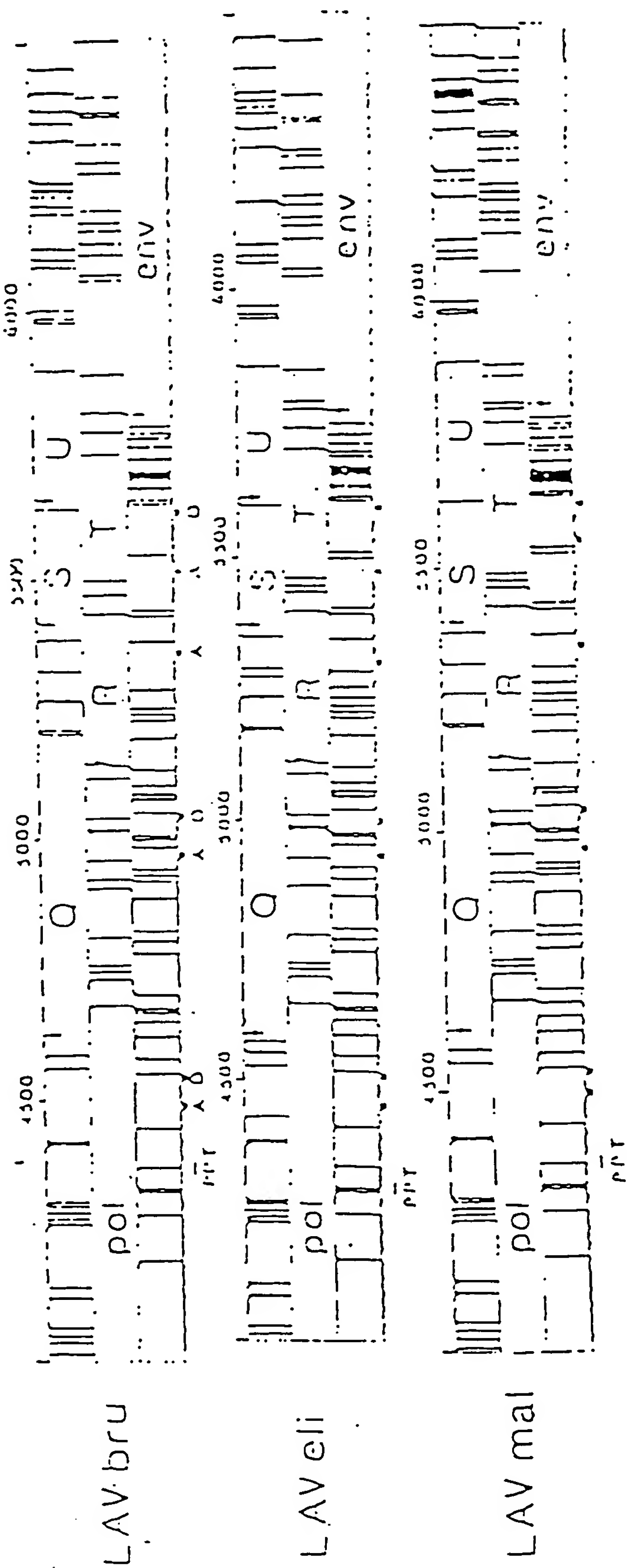


FIG. 3A

Coll
GG

GAG

```
                  10         20         30         40         50         60         70         80
LAV BRU   MGARASVLSG GELDRWEKIR LRPGGKKKYK LKHIVWASRE LERFAVNPGL LETSEGCRQI LGQLQPSLQT GSEELRSLYN
ARV 2                    K
LAV HAL               K  A               R    L            L        C    Q   HE   ST K      IK
LAV ELI               K  K               R               Y L           K  I     AI    T

                                                                 |p25
                  90        100        110        120        130        140        150        160
LAV BRU   TVATLYCVHQ RIEIKDTKEA LDKIEEEQNK SKKKAQQAAA ------DTGH SSQVSQNYPI VQNIQGQMVH QAISPRTLNA
ARV 2                  DV        E                    ----AAC  H               L
LAV HAL                DV        .    I     RQ T      AQQAAAA KH   S           A    I
LAV ELI            K G DV        E H                  ------   H H             L

                 170        180        190        200        210        220        230        240
LAV BRU   VVKVVEEKAF SPEVIPMFSA LSEGATPQDL NTMLNTVGGH QAAMQMLKET INEEAAEWDR VHPVHAGPIA PGQMREPRGS
ARV 2
LAV HAL       I                             H   I             D        D             P
LAV ELI       I                                                             L

                 250        260        270        280        290        300        310        320
LAV BRU   DIAGTTSTLQ EQIGWMTNNP PIPVGEIYKR WIILGLNKIV RMYSPTSILD IRQGPKEPFR DYVDRFYKTL RAEQASQEVK
ARV 2                                                                                         D
LAV HAL                     S        D                     V                      F         T
LAV ELI                 A   S                 V            V                                  D

                                                                 |p13
                 330        340        350        360        370        380        390        400
LAV BRU   NWMTETLLVQ NANPDCKTIL KALGPAATLE EMMTACQGVG GPGHKARVLA EAMSQVTNS- ATIMMQRGNF RNQRKIVKCF
ARV 2                                                                    F- H              T
LAV HAL                         C                  S              A   T A          KC - KI
LAV ELI                         Q                  S              A   V T A        KCP   I

                 410        420        430        440        450        460        470        480
LAV BRU   NCGKEGHIAR NCRAPRKKGC WKCGKEGHQM KDCTERQANF LGKIWPSYKG RPGNFLQSRP EPTAPPFLQS RPEPTAPPEE
ARV 2             K             R  R                                              ---- ---------
LAV HAL         L                                           H                     ---- ---------A
LAV ELI           K             R       L              R    H                     ---- ---------A

                 490        500        510
LAV BRU   SFRSGVETTT PSQKQEPIDK ELYPLTSLRS LFGNDPSSQ
ARV 2       F E K
LAV HAL    GF E IK-       QK        A  K       QL
LAV ELI    GF E I -       QK           K        L
```

FIG. 3B

Central region :

Q

```
                10          20          30          40          50          60          70          80
LAV BRU   MENRWQVMIV WQVDRMRIRT WKSLVKHHMY VSGKARGWFY RHHYESPHPR ISSEVHIPLG DARLVITTYW GLHTGERDWH
ARV 2                                      I K  K              T   V                 K          E
LAV MAL                           H          K  KH             R  K V                   VR    Q   K
LAV ELI       I            K                 K  HK                K              E      K         E

                90          100         110         120         130         140         150         160
LAV BRU   LGQGVSIEWR KKRYSTQVDP ELADQLIHLY YFDCFSDSAI RKALLGHIVS PRCEYQAGHN KVGSLQYLAL AALITPKKIK
ARV 2          A        K          G          H          E     KH I   YA                           T
LAV MAL     H        Q     L   D                     E      Q I              D            T    A    TR
LAV ELI               R        G          H          E         I   D                      T    A   Q

                170         180         190
LAV BRU   PPLPSVTKLT EDRWNKPQKT KGHRGSHTMN GH
ARV 2          K
LAV MAL        R          Q
LAV ELI        R          Q  R
```

R

```
                10          20          30          40          50          60          70          80
LAV BRU   MEQAPEDQGP QREPHNEWTL ELLEELKNEA VRHFPRIWLH GLGQHIYETY GDTWAGVEAI IRILQQLLFI HFRIGCRHSR
ARV 2                   Y                R          P     S   Y                                  Q
LAV MAL        A                         Q                S             E        S               Q
LAV ELI        A        Y   A            S                S             V                        Q

                90
LAV BRU   IGVTQQRRAR -NGASRS
ARV 2       II        R
LAV MAL     I R       -  S
LAV ELI     IIR       -  S
```

S (tat)

```
                10          20          30          40          50          60          70
LAV BRU   MEPVDPRLEP WKHPGSQPKT ACTTCYCKKC CFHCQVCFTT KALGISYGRK KRRQRRRPPQ GSQTHQVSLS KQ
ARV 2           H              R   HH                YA  R  G                  A    D    A
LAV MAL     D       N      N   R  P HK              Y  H  I  G                      H A  DP P E
LAV ELI     D       N      N   R  P HK H            Y  P  LH G                  G   C A   PIP
```

FIG. 3C

POL

```
                   10         20         30         40         50         60         70         80
LAV BRU    FFREDLAFLQ GKAREFSSEQ TRANSPTISS EQTRANSPTR RELQVWGRDN NSLSEAGADR QGTVSFNFPQ ITLWQRPLVT
ARV 2                                   --- ---------          GE
LAV HAL        H   P        P           --- ---------S    A   G - KT   T  E    I   S           V
LAV ELI        H   P     C L  PK        --- ---------S    A     -  P  KT  E
                                                                                                 A

                   90        100        110        120        130        140        150        160
LAV BRU    IKIGGQLKEA LLDTGADDTV LEEMSLPGRW KPKMIGGIGG FIKVRQYDQI LIEICGHKAI GTVLVGPTPV NIIGRNLLTQ
ARV 2       A                        W   K                        PV
LAV HAL    VRV                      IN  K
LAV ELI                                                                 K      I              H
                                     W   K                        P     Q

                  170        180        190        200        210        220        230        240
LAV BRU    IGGTLNFPIS PIETVPVKLK PGMDGPKVKQ WPLTEEKIKA LVEICTEMEK EGKISKIGPE NPYNTPVFAI KKKDSTKWRK
ARV 2
LAV HAL                                R               T    KD        L
LAV ELI                                                T     D         R           I

                  250        260        270        280        290        300        310        320
LAV BRU    LVDFRELNKR TQDFWEVQLG IPHPAGLKKK KSVTVLDVGD AYFSVPLDED FRKYTAFTIP SINNETPGIR YQYNVLPQGW
ARV 2        E                                                 K
LAV HAL
LAV ELI                                                                   S

                  330        340        350        360        370        380        390        400
LAV BRU    KGSPAIFQSS MTKILEPFRK QNPDIVIYQY MDDLYVGSDL EIGQHRTKIE ELRQHLLRWG LTTPDKKHQK EPPFLWMGYE
ARV 2
LAV HAL                        T X  E                                        F
LAV ELI                             EH                               E   K   I
                                                               K  E       F R

                  410        420        430        440        450        460        470        480
LAV BRU    LHPDKWTVQP IVLPEKDSWT VNDIQKLVGK LNWASQIYPG IKVRQLCKLL RGTKALTEVI PLTEEAELEL AENREILKEP
ARV 2                  H
LAV HAL                Q  D E                       A     K
LAV ELI             S  K    E         N  ER               K         A    DIV    A

                  490        500        510        520        530        540        550        560
LAV BRU    VHGVYYDPSK DLIAEIQKQG QGQWTYQIYQ EPFKNLKTGK YARMRGAHTN DVKQLTEAVQ KITTESIVIW GKTPKFKLPI
ARV 2        E          V
LAV HAL                                                   H                   VS         I
LAV ELI                           H           QY          IKS                  AQ            R
                                                         H             A     A S         A    R
```

```
                 570        580        590        600        610        620        630        640
LAV BRU   QKETWETWWT EYWQATWIPE WEFVNTPPLV KLWYQLEKEP IVGAETFYVD GAANRETKLG KAGYVTNRGR QKVVTLTDTT
ARV 2       I    A  H                                                H             D        SIA
LAV HAL         A                                  T                 H    X        D        S  E
LAV ELI            A                                    I            N             D        P

                 650        660        670        680        690        700        710        720
LAV BRU   NQKTELQAIY LALQDSGLEV NIVTDSQYAL GIIQAQPDKS ESELVNQIIE QLIKKEKVYL AWVPAHKGIG GNEQVDKLVS
ARV 2                                                       S
LAV HAL                     S                             I          Q D     S
LAV ELI            K

                 730        740        750        760        770        780        790        800
LAV BRU   AGIRKVLFLD GIDKAQDEHE KYHSNWRAMA SDFNLPPVVA KEIVASCDKC QLKGEAMHGQ VDCSPGIWQL DCTHLEGKVI
ARV 2              N       E                                                                   I
LAV HAL   S                E                      I                                            I
LAV ELI   Q                E       N

                 810        820        830        840        850        860        870        880
LAV BRU   LVAVHVASGY IEAEVIPAET GQETAYFLLK LAGRWPVKTI HTDNGSNFTS TTVKAACWWA GIKQEFGIPY NPQSQGVVES
ARV 2
LAV HAL   I                            I           VV            AA         N
LAV ELI                                            VV            AA

                 890        900        910        920        930        940        950        960
LAV BRU   MNKELKKIIG QVRDQAEHLK TAVQMAVFIH NFKRKGGIGG YSAGERIVDI IATDIQTKEL QKQITKIQNF RVYYRDSRDP
ARV 2       N                                                                                KK
LAV HAL                 E                                    I H                            H
LAV ELI                                        AR            I                  I

                 970        980        990       1000       1010
LAV BRU   LWKGPAKLLW KGEGAVVIQD NSDIKVVPRR KAKIIRDYGK QMAGDDCVAS RQDED
ARV 2
LAV HAL   I                                                    G G
LAV ELI   I                     K           V
```

FIG. 3D

ENV

```
                         SP                                          OMP
                 10         20         30 •|      40         50       • 60         70       • 80
LAV BRU   MRVK---EKY QHLWRWGWKW GTMLLGILMI CSATEKLWVT VYYGVPVWKE ATTTLFCASD AKAYDTEVHN VWATHACVPT
ARV 2      K  GTARN       ---- - L   M                                    R
LAV MAL      RELQRN  NV   --- -N     N  T  IA D                           S E        I
LAV ELI     ARGIEKN[] NV K --- -I       T   ADN                           S E  A     I

                 90        100        110        120      • 130      • 140        150        160
LAV BRU   DPNPQEVVLV NVTENFNMWK NDMVEQMHED IISLWDQSLK PCVKLTPLCV SLKCTDL-GN ATNTNSSNTN SSSGEMMME-
ARV 2              C               N    Q                      T N     - K         ---  ----KGKE I
LAV MAL           IE E      G      N                               T N  NVN T  V GTNAGS  RTNA IK  I
LAV ELI           IA E             N                               T N S E--L AN GTNG NV TIEEKG----

                •170        180        190        200        210 •      220        230      • 240
LAV BRU   KGEIKNCSFN ISTSIRGKVQ KEYAFFYKLD IIPIDNDTTS -----YTLTS CNTSVITQAC PKVSFEPIPI HYCAPAGFAI
ARV 2                T.   D I    N L  KI  VV     AS T  TNYTN R IU  R                       T
LAV MAL    - V       TPVGSD R  -  T  N  LVQ   DSDN  ----S K IN                   T D
LAV ELI    ---N      VT VLKD K QV  L  K   V      SST  -NSTN K IN    A

        •        250  •      260  •      270        280        290        300        310 •      320
LAV BRU   LKCNNKTFNG TGPCTNVSTV QCTHGIRPVV STQLLLNGSL AEEEVVIRSA NFTDNAKTII VQLNQSVEIN CTRPNNNTRK
ARV 2              K           I                     D   N              E  A
LAV MAL        D K    EI K          K                   IN  E L   T N     ET T       G     K
LAV ELI       RD K                                      I   E L N   N  AN E  K T  A  YQ    Q

                 330        340       •350        360        370        380        390      • 400
LAV BRU   SIRIQRGPGR AFVTIGK-IG NMRQAHCNIS RAKWNATLKQ IASKLREQFG NNKT-IIFKQ SSGGDPEIVT NSFNCGGEFF
ARV 2      Y --      N T AI   DI K         Q  N  E    VK            - V N              N     K
LAV MAL    C NF--   Q  LY T I-V DI R Y T N ETE DK  Q   V Y  GSLL- -   K  NS           T     R
LAV ELI    RTP -- L Q SLY TKS-RS IIG          Q SK  Q   V R  GTLL- -   I K  P          T

        •        410        420        430      •440        450        460 •      470        480
LAV BRU   YCNSTQLFNS TWFNSTWSTE GSNNTEGSDT ITLPCRIKQF INMWQEVGKA MYAPPISGQI RCSSNITGLL LTRDGGNN--
ARV 2        T    N  . -----RLN NTEG K N    I       I                   C    S             T -V
LAV MAL       TSK    Q NGAKL- -  S  STGS            I       KT          A Y  N L      I     NSSD
LAV ELI       TSG    NI A NNI TES NSTNTN      Q     I  K VAGR-    I    EAN  L                I --

                 490        500        510        520        530|       540 TMP    550        560
LAV BRU   NNGSEIFRPG GGDMRDNWRS ELYKYKVVKI EPLGVAPTKA KRRVVQREKR AVGI-GALFL GFLGAAGSTM GAASMTLTVQ
ARV 2     T DT V                         I          I                      V  N                 V L
LAV MAL   SDN TL               I        R                      E      I L-  N                 A L
LAV ELI   STN T                         Q          R          E      I L-  N                    V
```

FIG. 3E

```
                 570        580        590        600        610        620        630        640
LAV BRU   ARQLLSGIVQ QQNNLLRAIE AQQHLLQLTV WGIKQLQARI LAVERYLKDQ QLLGIWGCSG KLICTTAVPW NASWSNKSLE
ARV 2                                              V          R
LAV MAL                                            V          Q    R    H          H    F     S     R  D
LAV ELI         H                                                                  H    H     S     R  N

                 650        660        670        680        690        700        710        720
LAV BRU   QIWNNMTWME WDREINNYTS LIHSLIEESQ NQQEKNEQEL LELDKWASLW NWFNITNWLW YIKIFIMIVG GLVGLRIVFA
ARV 2     D  D  I  Q  E   D   K Y YT L                            S
LAV MAL   E        Q  EK  S   G I YN         I      K             S SK      R   IV     I    I
LAV ELI   E Q         E   D   G   Y          T      K             S  Q               I    I

                 730        740        750        760        770        780        790        800
LAV BRU   VLSIVNRVRQ GYSPLSFQTH LPTPRGP-DR PEGIEEEGGE RDRDRSIRLV NGSLALIWDD LRSLCLFSYH RLRDLLLIVT
ARV 2                          R   V    -     D                  V   D F     E         K          AA
LAV MAL       L               L L       F                    QG G        FS           H             A
LAV ELI       L                 L   A   -       T             G     V L  FS                     I AV

                 810        820        830        840        850        860        870
LAV BRU   RIVELLGRRG WEALKYWWNL LQYWSQELKN SAVSLLNATA IAVAEGTDRV IEVVQGACRA IRHIPRRIRQ GLERILL
ARV 2     T  I  K          S          I             W          T         A R Y    L  H          L
LAV MAL                  L          G          I     T         K         IG RPG   L           F  A
LAV ELI             DI   L                 R     S  FD I                  II K    VLN             S
```

FIG. 3F

F

```
                  10         20         30         40         50         60         70         80
LAV BRU   MGGKWSKSSV VGWPTVRERM K----RAEPA ADGVGAASR- ----DLEKHG AITSSNTAAT NAACAWLEAQ EE-EEVGFPV
ARV 2            R  H  G  SAI          RAEP              V  -  ----                    D          -
LAV MAL             I      KI    I   ----  TP  T  ET      V  QD AVSQ  D  E   AA   SP  N   S --- PP  E
LAV ELI             I      AI.   I   ----  TH              V  -  ----                S   D          SD

                  90        100        110        120        130        140        150        160
LAV BRU   TPQVPLRPMT YKAAVDLSHF LKEKGGLEGL IHSQRRQDIL DLWIYHTQGY FPDWQNYTPG PGVRYPLTFG WCYKLVPVEP
ARV 2     R              L I                    V     E                                I           F
LAV MAL   R            G F                D      VG  PK   E        V                     I  F        F     HS
LAV ELI   K            E L                       V  KK   E        V  H    I               I          E     D

                 170        180        190        200        210
LAV BRU   DKVEEANKGE NTSLLHPVSL HGMDDPEREV LEWRFDSRLA FHHVARELHP EYFKNC
ARV 2     E        E     K     H          E  A  K     V      K        H          Y  D
LAV MAL   EE       E    HG     I  Q       E  A        K  K    S      LR  R   Q      Y  D
LAV ELI   QE    DTE    TN      ICQ        E     Q      K   H          E  K   N      FY  -.
```

FIG. 4A

A

LAVbru vs.	GAG		POL		ENV Total		ENV OMP		ENV TMP	
HTLV-3 USA	512 0/0	0.8	1015 0/0	1.3	856 5/0	1.4	507 5/0	1.6	349 0/0	1.1
ARV-2 USA	502 12/2	3.4	1003 12/0	3.1	855 17/11	13.0	505 17/10	14.3	350 0/1	11.2
LAVeli Zaire	500 13/1	9.8	1002 13/0	5.5	853 22/14	20.7	504 22/14	25.3	349 0/0	13.8
LAVmal Zaire	505 14/7	12.0	1002 13/0	7.7	859 13/11	21.7	509 13/10	26.4	350 0/1	14.9

B

LAVeli vs.	GAG		POL		ENV Total		ENV OMP		ENV TMP	
LAVmal	505 1/6	10.8	1002 0/0	8.4	859 13/11	19.8	509 8/13	23.6	350 0/1	14.3

FIG. 4B

A

L'AVbru vs.	orf F		central region: orf Q		orf R		orf S	
HTLV-3 (USA)	206 0/0	1.5	192 0/0	0	[illegible]	nd	80 0/0	2.5
ARV-2 (USA)	210 0/4	12.6	192 0/0	10.0	97 0/1	9.4	81 0/1	15.0
LAVeli (Zaire)	206 1/1	19.4	192 0/0	10.4	96 0/0	11.5	80 0/0	27.5
LAVmal (Zaire)	209 2/5	27.0	192 0/0	12.6	96 0/0	10.4	80 0/0	23.8

B

LAVeli vs.	orf F		orf Q		orf R		orf S	
LAVmal	209 3/6	22.5	192 0/0	12.0	96 0/0	6.3	80 0/0	11.3

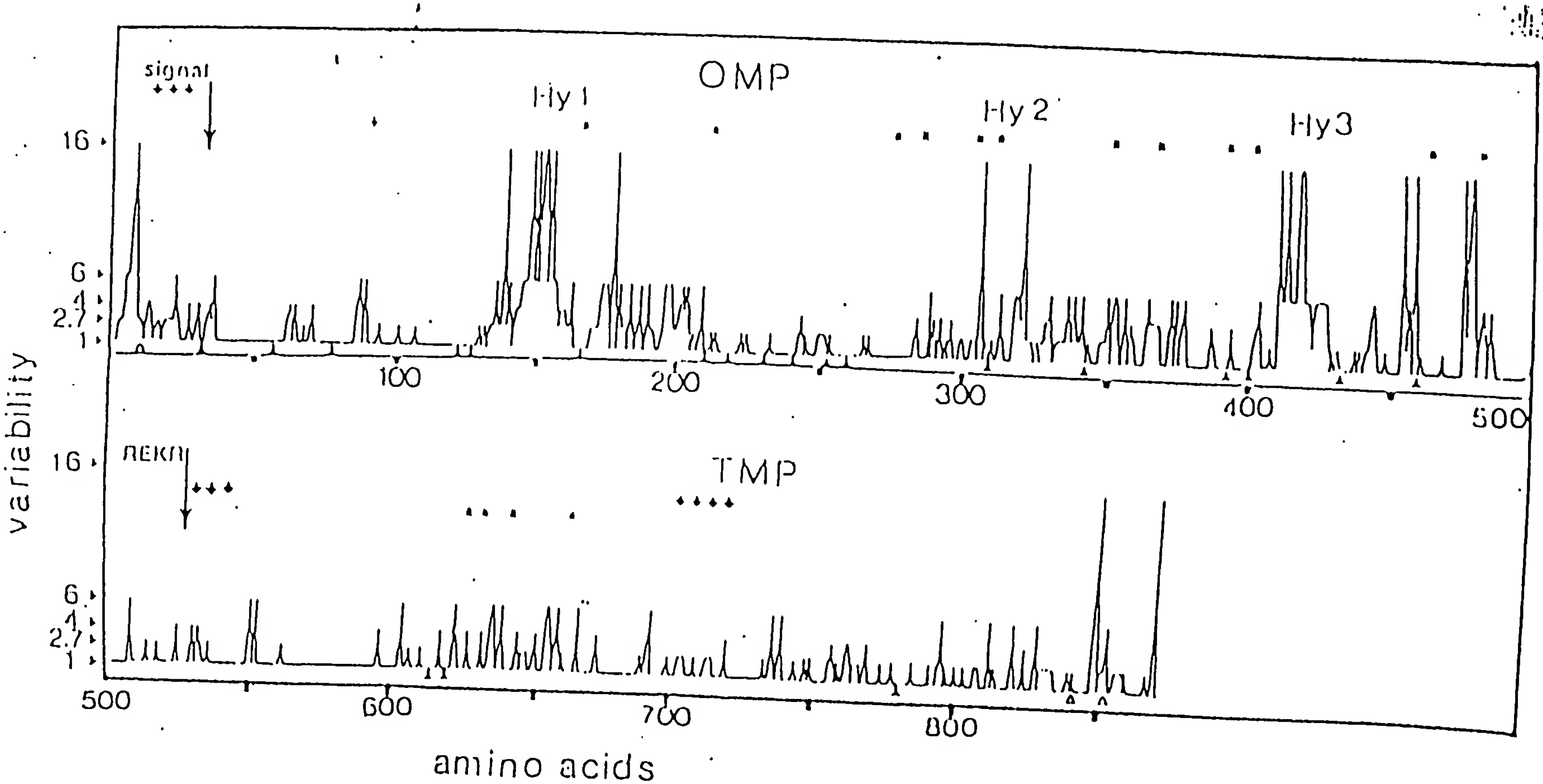

OMP
signal
Hy 1
Hy 2
Hy3
TMP
16
6
4
2.7
1
100
200
300
400
500
600
700
800
variability
amino acids

FIG. 5

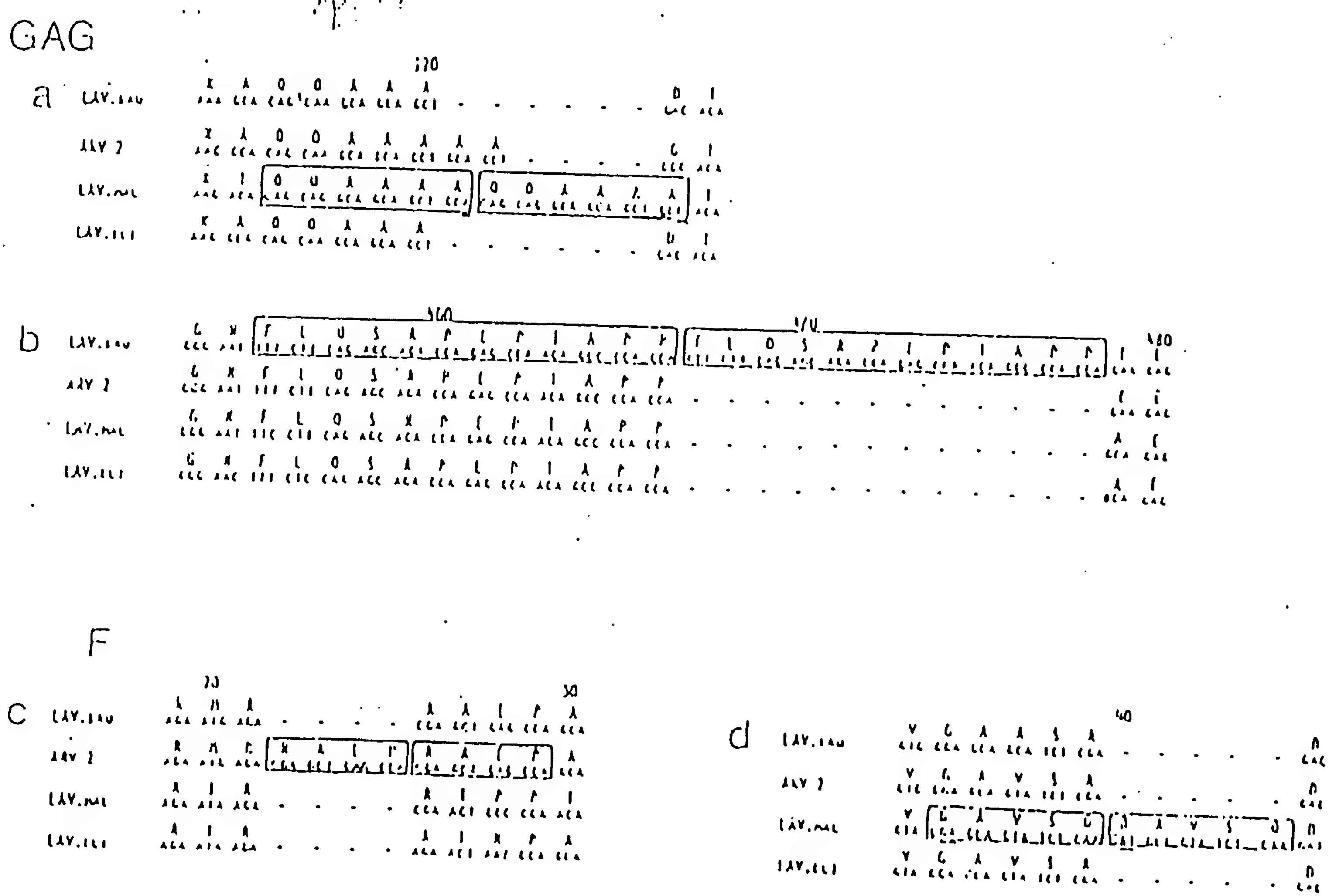
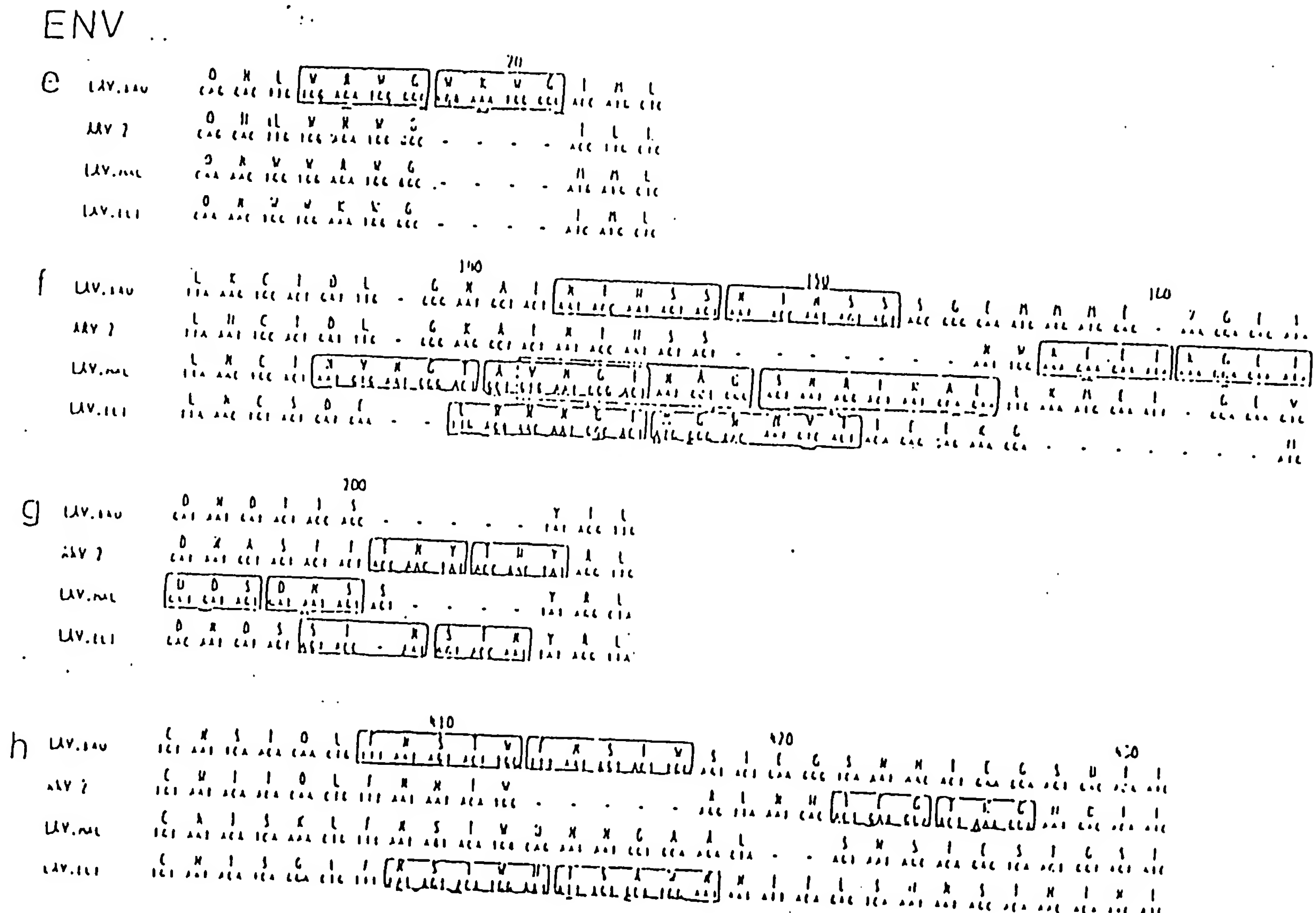


FIG. 6A



ENV
e
f
g
h
LAV.BRU
ARV 2
LAV.MAL
LAV.ELI
70
140
150
160
200
410
420
430

FIG. 63

FIG. 7A

LAV.HAE

→R

GGTCTCTCTTGTTAGACCAGGTCGAGCCCGGGAGCTCTCTGGCTAGCAAGGAACCCACTG

R ↔ U5.

CTTAAGCCTCAATAAAGCTTGCCTTGAGTGCCTCAAGCAGTGTGTGCCCATCTGTTGTGT

100

U5 ←

GACTCTGGTAACTAGAGATCCCTCAGACCACTCTAGACGGTGTAAAAATCTCTAGCAGTG

GCGCCCGAACAGGGACTTTAAAGTGAAAGTAACAGGGACTCGAAAGCGGAAGTTCCAGAG

200

AACTTCTCTCGACGCAGGACTCGGCTTGCTGAGGTGCACACAGCAAGAGGCGAGAGCGGC

→GAG 300

MetGlyAlaArg

GACTGGTGAGTACGCCAATTTTTGACTAGCGGAGGCTAGAAGGAGAGAGATGGGTGCGAG

AlaSerValLeuSerGlyGlyLysLeuAspAlaTrpGluLysIleArgLeuArgProGly

AGCGTCAGTATTAAGCGGGGGAAAATTAGATGCATGGGAGAAAATTCGGTTAAGGCCAGG

400

GlyLysLysLysTyrArgLeuLysHisLeuValTrpAlaSerArgGluLeuGluArgPhe

GGGAAAGAAAAAATATAGACTGAAACATTTAGTATGGGCAAGCAGGGAGCTGGAAAGATT

AlaLeuAsnProGlyLeuLeuGluThrGlyGluGlyCysGlnGlnIleMetGluGlnLeu

CGCACTTAACCCTGGCCTTTTAGAAACAGGAGAAGGATGTCAACAAATAATGGAACAGCT

500

GlnSerThrLeuLysThrGlySerGluGluIleLysSerLeuTyrAsnThrValAlaThr

ACAATCAACTCTCAAGACAGGATCAGAAGAAATTAAATCATTATATAATACAGTAGCAAC

600

LeuTyrCysValHisGlnArgIleAspValLysAspThrLysGluAlaLeuAspLysIle

CCTCTATTGTGTACATCAAAGGATAGATGTAAAAGACACCAAGGAAGCGCTAGATAAAAT

GluGluIleGlnAsnLysSerArgGlnLysThrGlnGlnAlaAlaAlaAlaGlnGlnAla

AGAGGAAATACAAAATAAGAGCAGGCAAAAGACACAGCAGGCAGCAGCTGCACAGCAGGC

700

AlaAlaAlaThrLysAsnSerSerSerValSerGlnAsnTyrProIleValGlnAsnAla

AGCAGCTGCCACAAAAAACAGCAGCAGTGTCAGTCAAAATTACCCCATAGTGCAAAATGC

GlnGlyGlnMetIleHisGlnAlaIleSerProArgThrLeuAsnAlaTrpValLysVal

ACAAGGGCAAATGATACATCAGGCCATATCACCTAGGACTTTGAATGCATGGGTGAAAGT

800

IleIleGluLysAlaPheSerProGluValIleProMetPheSerAlaLeuSerGluGly

AATACAAAGAAAAGGCTTTCAGCCCAGAAGTGATACCCATGTTCTCAGCATTATCAGAGGG

900

AlaThrProGlnAspLeuAsnMetMetLeuAsnIleValGlyGlyHisGlnAlaAlaMet

GGCCACCCCACAAGATTTAAATATGATGCTGAACATAGTTGGAGGACACCAGGCAGCTAT

GlnMetLeuLysAspThrIleAsnGluGluAlaAlaAspTrpAspArgValHisProVal

GCAAATGTTAAAAGATACCATCAATGAGGAAGCTGCAGACTGGGACAGGGTACATCCAGT

1000

HisAlaGlyProIleProProGlyGlnMetArgGluProArgGlySerAspIleAlaGly

ACATGCAGGGCCTATTCCCCCAGGCCAGATGAGAGAACCAAGAGGAAGTGACATAGCAGG

FIG. 7B

Thr[illegible]ThrLeuGlnGluGlnIleGlyTrpMetThrSerAsnProProIleProVal

AACTA[illegible]TACCCTTCAAGAACAAATAGGATGGATGACAAGCAACCCACCTATCCCAGT

1100

GlyAspIleTyrLysArgTrpIleIleLeuGlyLeuAsnLysIleValArgMetTyrSer

GGGAGACATCTATAAAAGATGGATAATCCTGGGATTAAATAAAATAGTAAGAATGTATAG

1200

ProValSerIleLeuAspIleArgGlnGlyProLysGluProPheArgAspTyrValAsp

CCCTGTCAGCATTTTGGACATAAGACAAGGGCCAAAGGAACCTTTTAGAGACTATGTAGA

ArgPhePheLysThrLeuArgAlaGluGlnAlaThrGlnGluValLysAsnTrpMetThr

TAGGTTCTTTAAAACTCTCAGAGCTGAGCAAGCTACACAGGAGGTAAAAAATTGGATGAC

1300

GluThrLeuLeuValGlnAsnAlaAsnProAspCysLysThrIleLeuLysAlaLeuGly

AGAAACCTTGCTGGTCCAAAATGCGAATCCAGACTGTAAGACCATTTTAAAAGCATTAGG

ProGlyAlaThrLeuGluGluMetMetThrAlaCysGlnGlyValGlyGlyProSerHis

ACCAGGGGCTACATTAGAAGAAATGATGACAGCATGCCAGGGAGTGGGAGGACCCAGTCA

1400

LysAlaArgValLeuAlaGluAlaMetSerGlnAlaThrAsnSerThrAlaAlaIleMet

TAAAGCAAGAGTTTTGGCTGAGGCAATGAGCCAAGCAACAAATTCAACTGCTGCCATAAT

1500

MetGlnArgGlyAsnPheLysGlyGlnLysArgIleLysCysPheAsnCysGlyLysGlu

GATGCAGAGAGGTAATTTTAAGGGCCAGAAAAGAATTAAGTGTTTCAACTGTGGCAAAGA

GlyHisLeuAlaArgAsnCysArgAlaProArgLysLysGlyCysTrpLysCysGlyLys

AGGACACCTAGCCAGAAATTGCAGGGCCCCTAGGAAAAAGGGCTGTTGGAAATGTGGAA

1600

→POL

PhePheArgGluAsnLeu

GluGlyHisGlnMetLysAspCysThrGluArgGlnAlaAsnPheLeuGlyLysIleTrp

GGAAGGACACCAAATGAAAGACTGCACTGAGAGACAGGCTAATTTTTTAGGGAAAATTTG

AlaPheProGlnGlyLysAlaArgGluPheProSerGluGlnThrArgAlaAsnSerPro

ProSerHisLysGlyArgProGlyAsnPheLeuGlnSerArgProGluProThrAlaPro

GCCTTCCCACAAGGGAAGGCCAGGGAATTTCCTTCAGAGCAGACCAGAGCCAACAGCCCC

1700

ThrSerArgGluLeuArgValTrpGlyGlyAspLysThrLeuSerGluThrGlyAlaGlu

ProAlaGluSerPheGlyPheGlyGluGluIleLysProSerGlnLysGlnGluGlnLys

ACCAGCAGAGAGCTTCGGGTTTGGGGAGGAGATAAAACCCTCTCAGAAACAGGAGCAGAA

1800

ArgG[illegible]GlyIleValSerPheSerPheProGlnIleThrLeuTrpGlnArgProValVal

As[illegible]GluLeuTyrProLeuAlaSerLeuLysSerLeuPheGlyAsnAspGlnLeuSer

AGA[illegible]GGAATTGTATCCTTTAGCTTCCCTCAAATCACTCTTTGGCAACGACCAGTTGTC

GAG

ThrValArgValGlyGlyGlnLeuLysGluAlaLeuLeuAspThrGlyAlaAspAspThr

Gln

ACACTAAGAGTAGGAGGACAGCTAAAAGAAGCTCTATTAGACACAGGAGCAGATGATACA

1900

ValLeuGluGluIleAsnLeuProGlyLysTrpLysProLysMetIleGlyGlyIleGly

GTATTAGAAGAAATAAATTTGCCAGGAAAATGGAAACCAAAAATGATAGGGGGAATTGGA

GlyPheIleLysValArgGlnTyrAspGlnIleLeuIleGluIleCysGlyLysLysAla

GGTTTTATCAAAGTAAGACAGTATGATCAAATACTTATAGAAATTTGTGGAAAAAGGCT

2000

FIG. 7C

IleGlyThrIleLeuValGlyProThrProValAsnIleIleGlyArgAsnMetLeuThr

ATAGGTACAATATTGGTAGGACCTACACCTGTCAACATAATTGGACGAAATATGTTGACT

GlnIleGlyCysThrLeuAsnPheProIleSerProIleGluThrValProValLysLeu 2100

CAGATTGGTTGTACTTTAAATTTTCCAATTAGTCCTATTGAGACTGTACCAGTAAAATTA

LysProGlyMetAspGlyProArgValLysGlnTrpProLeuThrGluGluLysIleLys

AAGCCAGGGATGGATGGCCCAAGGGTTAAACAATGGCCATTGACAGAAGAAAAAATAAAA

2200

AlaLeuThrGluIleCysLysAspMetGluLysGluGlyLysIleLeuLysIleGlyPro

GCATTAACAGAAATTTGTAAAGATATGGAAAAGGAAGGAAAAATTTTAAAAATTGGGCCT

GluAsnProTyrAsnThrProValPheAlaIleLysLysLysAspSerThrLysTrpArg

GAAAATCCATACAATACTCCAGTATTTGCCATAAAGAAAAAAGACAGCACTAAATGGAGA

2300

LysLeuValAsnPheArgGluLeuAsnLysArgThrGlnAspPheTrpGluValGlnLeu

AAATTAGTGAATTTCAGAGAGCTTAATAAAAGAACTCAAGATTTTTGGGAAGTTCAATTA

GlyIleProHisProAlaGlyLeuLysLysLysLysSerValThrValLeuAspValGly 2400

GGAATACCACATCCTGCTGGGTTGAAAAAGAAAAAATCAGTCACAGTATTGGATGTGGGG

AspAlaTyrPheSerValProLeuAspGluAspPheArgLysTyrThrAlaPheThrIle

GATGCATATTTTTCAGTCCCTTTAGATGAAGATTTCAGGAAGTATACTGCATTCACTATA

2500

ProSerIleAsnAsnGluThrProGlyIleArgTyrGlnTyrAsnValLeuProGlnGly

CCCAGTATTAATAATGAGACACCAGGGATTAGATATCAGTACAATGTGCTACCACAGGGA

TrpLysGlySerProAlaIlePheGlnSerSerMetThrLysIleLeuGluProPheArg

TGGAAAGGATCACCAGCAATATTCCAGAGTAGCATGACAAAAATCTTAGAACCCTTTAGA

2600

ThrLysAsnProGluIleValIleTyrGlnTyrMetAspAspLeuTyrValGlySerAsp

ACAAAAAATCCAGAAATAGTCATATACCAATACATGGATGATTTGTATGTAGGGTCTGAT

LeuGluIleGlyGlnHisArgThrLysIleGluGluLeuArgGluHisLeuLeuLysTrp 2700

TTAGAAATAGGACAACATAGAACAAAAATAGAGGAACTAAGAGAACATCTATTGAAATGG

GlyPheThrThrProAspLysLysHisGlnLysGluProProPheLeuTrpMetGlyTyr

GGATTTACCACACCAGACAAAAAGCATCAGAAAGAACCCCCATTTCTTTGGATGGGGTAT

2800

GluLeuHisProAspLysTrpThrValGlnProIleGlnLeuProAspLysGluSerTrp

GAACTGCACCCTGACAAATGGACAGTGCAGCCTATACAACTGCCAGACAAGGAAAGCTGG

ThrValAsnAspIleGlnLysLeuValGlyLysLeuAsnTrpAlaSerGlnIleTyrPro

ACTGTCAATGATATACAGAAATTGGTGGGAAAACTAAATTGGGCAAGTCAGATTTATCCA

2900

GlyIleLysValLysGlnLeuCysLysLeuLeuArgGlyAlaLysAlaLeuThrAspIle

GGAATTAAAGTAAAGCAATTATGTAAACTCCTTAGGGGAGCAAAAGCACTAACAGACATA

ValProLeuThrAlaGluAlaGluLeuGluLeuAlaGluAsnArgGluIleLeuLysGlu 3000

GTACCATTAACTGCAGAGGCAGAATTAGAATTGGCAGAGAACAGGGAAATTCTAAAAGAA

FIG. 7D

ProValHisGlyValTyrTyrAspProSerLysAspLeuIleAlaGluIleGlnLysGln
CCAGTCCATGGGGTATATTATGACCCATCAAAAGACTTAATAGCAGAAATACAGAAGCAG
3100

GlyGlnGlyGlnTrpThrTyrGlnIleTyrGlnGluGlnTyrLysAsnLeuLysThrGly
GGGCAAGGTCAATGGACATATCAAATATACCAAGAGCAATATAAAAATCTGAAAACAGGG

LysTyrAlaArgIleLysSerAlaHisThrAsnAspValLysGlnLeuThrGluAlaVal
AAGTATGCAAGAATAAAGTCTGCCCACACTAATGATGTAAAACAATTAACAGAAGCAGTG
3200

GlnLysIleAlaGlnGluSerIleValIleTrpGlyLysThrProLysPheArgLeuPro
CAAAAGATAGCCCAAGAAAGCATAGTAATATGGGGAAAAACTCCTAAATTTAGACTACCC

IleGlnLysGluThrTrpGluAlaTrpTrpThrGluTyrTrpGlnAlaThrTrpIlePro
3300
ATACAAAAAGAAACATGGGAGGCATGGTGGACAGAATATTGGCAAGCCACCTGGATCCCT

GluTrpGluPheValAsnThrProProLeuValLysLeuTrpTyrGlnLeuGluThrGlu
GAATGGGAGTTTGTCAATACTCCTCCCCTAGTAAAACTATGGTACCAGTTAGAAACAGAA
3400

ProIleValGlyAlaGluThrPheTyrValAspGlyAlaAlaAsnArgGluThrLysLys
CCCATAGTAGGAGCAGAAACTTTCTATGTAGATGGGGCAGCTAATAGAGAAACTAAAAAG

GlyLysAlaGlyTyrValThrAspArgGlyArgGlnLysValValSerLeuThrGluThr
GGAAAAGCAGGATATGTTACTGACAGAGGAAGACAAAAGGTTGTCTCCTTAACTGAAACA
3500

ThrAsnGlnLysThrGluLeuGlnAlaIleHisLeuAlaLeuGlnAspSerGlySerGlu
ACAAATCAGAAGACTGAATTACAAGCAATCCACTTAGCTTTACAGGATTCAGGATCAGAA

ValAsnIleValThrAspSerGlnTyrAlaLeuGlyIleIleGlnAlaGlnProAspLys
3600
GTAAACATAGTAACAGACTCACAGTATGCATTAGGGATTATTCAAGCACAACCAGATAAA

SerGluSerGluIleValAsnGlnIleIleGluGlnLeuIleGlnLysAspLysValTyr
AGTGAATCAGAGATTGTTAATCAAATAATAGAGCAATTAATACAGAAGGACAAGGTCTAC
3700

LeuSerTrpValProAlaHisLysGlyIleGlyGlyAsnGluGlnValAspLysLeuVal
CTGTCATGGGTACCAGCACACAAAGGGATTGGAGGAAATGAACAAGTAGATAAATTAGTC

SerSerGlyIleArgLysValLeuPheLeuAspGlyIleAspLysAlaGlnGluGluHis
AGCAGTGGAATCAGAAAGGTACTATTTTTAGATGGGATAGATAAGGCTCAAGAAGAACAT
3800

GluLysTyrHisSerAsnTrpArgAlaMetAlaSerAspPheAsnLeuProProIleVal
GAAAAGTATCACAGCAATTGGAGAGCAATGGCTAGTGACTTTAATCTACCACCTATAGTA

AlaLysGluIleValAlaSerCysAspLysCysGlnLeuLysGlyGluAlaMetHisGly
3900
GCGAAGGAAATAGTAGCCAGCTGTGATAAATGTCAACTAAAAGGGGAAGCCATGCATGGA

GlnValAspCysSerProGlyIleTrpGlnLeuAspCysThrHisLeuGluGlyLysIle
CAAGTAGACTGTAGTCCAGGGATATGGCAATTAGATTGCACACATCTAGAAGGAAAAATA
4000

IleIleValAlaValHisValAlaSerGlyTyrIleGluAlaGluValIleProAlaGlu
ATCATAGTAGCAGTCCATGTAGCCAGTGGATATATAGAAGCAGAAGTTATCCCAGCAGAA

ThrGlyGlnGluThrAlaTyrPheIleLeuLysLeuAlaGlyArgTrpProValLysVal
ACAGGACAGGAGACAGCATACTTTATACTAAAATTAGCAGGAAGATGGCCAGTAAAAGTA
4100

FIG. 7E

```
Val[illegible]AspAsnGlySerAsnPheThrSerAlaAlaValLysAlaAlaCysTrpTrp
GTAC[illegible]AGACAATGGCAGCAATTTCACCAGTGCTGCAGTTAAAGCAGCCTGTTGGTGG
                                                                4200
AlaAsnIleLysGlnGluPheGlyIleProTyrAsnProGlnSerGlnGlyValValGlu
GCAAATATCAAACAGGAATTTGGAATTCCCTACAACCCCCAAAGTCAAGGAGTAGTGGAA

SerMetAsnLysGluLeuLysLysIleIleGlyGlnValArgGluGlnAlaGluHisLeu
TCTATGAATAAGGAATTAAAGAAAATCATAGGGCAGGTAAGAGAGCAAGCTGAACACCTT
                                            4300
LysThrAlaValGlnMetAlaValPheIleHisAsnPheLysArgLysGlyGlyIleGly
AAGACAGCAGTACAAATGGCAGTGTTCATTCACAATTTTAAAAGAAAAGGGGGGATTGGG

GlyTyrSerAlaGlyGluArgIleIleAspMetIleAlaThrAspIleGlnThrLysGlu
GGGTACAGTGCAGGGGAAAGAATAATAGACATGATAGCAACAGACATACAAACTAAAGAA-
            4400
LeuGlnLysGlnIleThrLysIleGlnAsnPheArgValTyrTyrArgAspAsnArgAsp
TTACAAAAACAAATTACAAAAATTCAAAATTTTCGGGTTTATTACAGGGACAACAGAGAC
                                                                4500
ProIleTrpLysGlyProAlaLysLeuLeuTrpLysGlyGluGlyAlaValValIleGln
CCAATTTGGAAAGGACCAGCAAAACTACTCTGGAAAGGTGAAGGGGCAGTAGTAATACAG
                                                                Q
AspAsnSerAspIleLysValValProArgArgLysAlaLysIleIleArgAspTyrGly
                                                                MetGlu
GACAATAGTGATATAAAGGTAGTACCAAGAAGAAAAGCAAAAATCATTAGGATTATGGA
                                            4600       POL
LysGlnMetAlaGlyAspAspCysValAlaGlyGlyGlnAspGluAsp
 AsnArgTrpGlnValMetIleValTrpGlnValAspArgMetArgIleArgThrTrpHis
AAACAGATGGCAGGTGATGATTGTGTGGCAGGTGGACAGGATGAGGATTAGAACATGGCA

SerLeuValLysHisHisMetTyrValSerLysLysAlaLysAsnTrpPheTyrArgHis
CAGTTTAGTAAAACATCATATGTATGTCTCAAAGAAAGCTAAAAATTGGTTTTATAGACA
            4700
HisTyrGluSerArgHisProLysValSerSerGluValHisIleProLeuGlyAspAla
TCACTATGAAAGCAGGCATCCAAAAGTAAGTTCAGAAGTACACATCCCACTAGGGGATGC
                                                                4800
ArgLeuValValArgThrTyrTrpGlyLeuGlnThrGlyGluLysAspTrpHisLeuGly
TAGATTAGTAGTAAGAACATATTGGGGTCTGCAAACAGGAGAAAAAGACTGGCACTTGGG

HisGlyValSerIleGluTrpArgGlnLysArgTyrSerThrGlnLeuAspProAspLeu
TCATGGGGTCTCCATAGAATGGAGGCAGAAAAGATATAGCACACAACTAGATCCTGACCT
                                            4900
Al[illegible]pGlnLeuIleHisLeuTyrTyrPheAspCysPheSerGluSerAlaIleArgGln
AGC[illegible]ACCAACTGATTCATCTGTACTATTTTGATTGTTTTTCAGAATCTGCCATAAGACA

AlaIleLeuGlyHisIleValSerProArgCysAspTyrGlnAlaGlyHisAsnLysVal
AGCCATATTAGGACATATAGTTAGTCCTAGGTGTGATTATCAAGCAGGACATAACAAGGT
            5000
GlySerLeuGlnTyrLeuAlaLeuThrAlaLeuIleAlaProLysLysThrArgProPro
AGGATCTTTACAGTATTTGGCACTAACAGCATTAATAGCACCAAAAAAGACAAGGCCACC
                                           R                    5100
                                           MetGluGlnAlaProAlaAspGlnGly
LeuProSerValArgLysLeuThrGluAspArgTrpAsnLysProGlnGlnThrLysGly
TTTGCCTAGTGTTAGGAAGCTAACAGAAGATAGATGGAACAAGCCCCAGCAGACCAAGGG
```

FIG. 7F

```
                                          Q<-
ProGlnArgGluProHisAsnGluTrpThr|LeuGluLeuLeuGluGluLeuLysGlnGlu
 HisArgGlySerHisThrMetAsnGlyHis|
CCACAGAGGGAGCCACACAATGAATGGACA|TTAGAACTTTTAGAGGAGCTTAAGCAAGAA
                                        5200
AlaValArgHisPheProArgIleTrpLeuHisSerLeuGlyGlnHisIleTyrGluThr
GCTGTCAGACACTTTCCTAGGATATGGCTCCATAGTTTAGGACAACATATCTATGAAACT

TyrGlyAspThrTrpGluGlyValGluAlaIleIleArgSerLeuGlnGlnLeuLeuPhe
TATGGGGATACCTGGGAAGGAGTTGAAGCTATAATAAGAAGTCTGCAACAACTGCTGTTT
                5300
IleHisPheArgIleGlyCysGlnHisSerArgIleGlyIleThrArgGlnArgArgAla
ATTCATTTCAGAATTGGGTGTCAACATAGCAGAATAGGCATTACTCGACAGAGAAGAGCA
      ->S          R<-                                   5400
ArgAsnGlySerSerArgSer|
   MetAspProValAspProAsnLeuGluProTrpAsnHisProGlySerGlnProArg
AGAAATGGATCCAGTAGATCC|TAACTTAGAGCCCTGGAACCATCCAGGCAGTCAGCCTAG

ThrProCysAsnLysCysTyrCysLysLysCysCysTyrHisCysGlnMetCysPheIle
GACGCCTTGTAATAAGTGTTATTGTAAAAAGTGCTGCTATCATTGCCAAATGTGCTTCAT
                                      5500
ThrLysGlyLeuGlyIleSerTyrGlyArgLysLysArgArgGlnArgArgArgProPro
AACGAAAGGCTTAGGCATCTCCTATGGCAGGAAGAAGCGGAGACAGCGACGAAGACCTCC
                                        S<-
GlnGlyAsnGlnAlaHisGlnAspProLeuProGluGln|
TCAGGGCAATCAGGCTCATCAAGATCCTCTACCAGAGCAG|TAAGTAGTATATGTAATACA
              5600
ACCTTTAGTGATATTAGCAATAGTAGCATTAGTAGTAACGCTAATAATAGCAATAGTTGT
                                                         5700
GTGGACCATAGTATTTATAGAAATTAGGAAAATAAGAAGACAAAGGAAAATAGACAGGTT
                                         ->ENV
                                         MetArgValArgGluIleGlnArg
GATTGATAGAATAAGAGAAAGAGCAGAAGATAGTGGCA|ATGAGAGTGAGGGAGATACAGA
                                       5800
AsnTyrGlnAsnTrpTrpArgTrpGlyMetMetLeuLeuGlyMetLeuMetThrCysSer
GGAATTATCAAAACTGGTGGAGATGGGGCATGATGCTCCTTGGGATGTTGATGACCTGTA

IleAlaGluAspLeuTrpValThrValTyrTyrGlyValProValTrpLysGluAlaThr
GTATTGCACAAGATTTGTGGGTTACAGTTTATTATGGGGTACCTGTGTGGAAAGAAGCAA
                5900
Thr[illegible]LeuPheCysAlaSerAspAlaLysSerTyrGluThrGluValHisAsnIleTrp
CCACT[illegible]CTATTTTGTGCATCAGATGCTAAATCATATGAAACAGAAGTACATAACATCT
                                                         6000
AlaThrHisAlaCysValProThrAspProAsnProGlnGluIleGluLeuGluAsnVal
GGGCTACACATGCCTGTGTACCCACGGACCCCAACCCACAAGAAATAGAACTGGAAAATG

ThrGluGlyPheAsnMetTrpLysAsnAsnMetValGluGlnMetHisGluAspIleIle
TCACAGAAGGGTTTAACATGTGGAAAAATAACATGGTGGAGCAGATGCATGAGGATATAA
                                      6100
```

FIG. 7G

SerLeuTrpAspGlnSerLeuLysProCysValLysLeuThrProLeuCysValThrLeu
TCAGT[illegible]GGATCAAAGCCTAAAACCATGTGTAAAGCTAACCCCACTCTGTGTCACTT

AsnCysThrAsnValAsnGlyThrAlaValAsnGlyThrAsnAlaGlySerAsnArgThr
TAAACTGCACTAATGTGAATGGGACTGCTGTGAATGGGACTAATGCTGGGAGTAATAGGA
6200

AsnAlaGluLeuLysMetGluIleGlyGluValLysAsnCysSerPheAsnIleThrPro
CTAATGCAGAATTGAAAATGGAAATTGGAGAAGTGAAAAACTGCTCTTTCAATATAACCC

6300
ValGlySerAspLysArgGlnGluTyrAlaThrPheTyrAsnLeuAspLeuValGlnIle
CAGTAGGAAGTGATAAAAGGCAAGAATATGCAACTTTTTATAACCTTGATCTAGTACAAA

AspAspSerAspAsnSerSerTyrArgLeuIleAsnCysAsnThrSerValIleThrGln
TAGATGATAGTGATAATAGTAGTTATAGGCTAATAAATTGTAATACCTCAGTAATTACAC
6400

AlaCysProLysValThrPheAspProIleProIleHisTyrCysAlaProAlaGlyPhe
AGGCTTGTCCAAAGGTAACCTTTGATCCAATTCCCATACATTATTGTGCCCCAGCTGGTT

AlaIleLeuLysCysAsnAspLysLysPheAsnGlyThrGluIleCysLysAsnValSer
TTGCAATTCTAAAGTGTAATGATAAGAAGTTCAATGGAACGGAAATATGTAAAAATGTCA
6500

ThrValGlnCysThrHisGlyIleLysProValValSerThrGlnLeuLeuLeuAsnGly
GTACAGTACAATGTACACATGGAATTAAGCCAGTGGTGTCAACTCAACTGCTGTTAAATG

6600
SerLeuAlaGluGluGluIleMetIleArgSerGluAsnLeuThrAspAsnThrLysAsn
GCAGTCTAGCAGAAGAAGAGATAATGATTAGATCTGAAAATCTCACAGACAATACTAAAA

IleIleValGlnLeuAsnGluThrValThrIleAsnCysThrArgProGlyAsnAsnThr
ACATAATAGTACAGCTTAATGAAACTGTAACAATTAATTGTACAAGGCCTGGAAACAATA
6700

ArgArgGlyIleHisPheGlyProGlyGlnAlaLeuTyrThrThrGlyIleValGlyAsp
CAAGAAGAGGGATACATTTCGGCCCAGGGCAAGCACTCTATACAACAGGGATAGTAGGAG

IleArgArgAlaTyrCysThrIleAsnGluThrGluTrpAspLysThrLeuGlnGlnVal
ATATAAGAAGAGCATATTGTACTATTAATGAAACAGAATGGGATAAAACTTTACAACAGG
6800

AlaValLysLeuGlySerLeuLeuAsnLysThrLysIleIlePheAsnSerSerSerGly.
TAGCTGTAAAACTAGGAAGCCTTCTTAACAAAACAAAAATAATTTTTAATTCATCCTCAG

6900
GlyAspProGluIleThrThrHisSerPheAsnCysArgGlyGluPhePheTyrCysAsn
GAGGGGACCCAGAAATTACAACACACAGTTTTAATTGTAGAGGGGAATTTTTCTACTGTA

Thr~~Ser~~LysLeuPheAsnSerThrTrpGlnAsnAsnGlyAlaArgLeuSerAsnSerThr
ATACATCAAAACTGTTTAATAGTACATGGCAGAATAATGGTGCAAGACTAAGTAATAGCA
7000

GluSerThrGlySerIleThrLeuProCysArgIleLysGlnIleIleAsnMetTrpGln
CAGAGTCAACTGGTAGTATCACACTCCCATGCAGAATAAAACAAATTATAAATATGTGGC

LysThrGlyLysAlaMetTyrAlaProProIleAlaGlyValIleAsnCysLeuSerAsn
AGAAAACAGGAAAAGCTATGTATGCCCCTCCCATCGCAGGAGTCATCAACTGTTTATCAA
7100

IleThrGlyLeuIleLeuThrArgAspGlyGlyAsnSerSerAspAsnSerAspAsnGlu
ATATTACAGGGCTGATATTAACAAGAGATGGTGGAAATAGTAGTGACAATAGTGACAATG

7200

FIG. 7H

ThrLeuArgProGlyGlyGlyAspMetArgAspAsnTrpIleSerGluLeuTyrLysTyr
AGACCTTAAGACCTGCAGGAGGAGATATGAGGGACAATTGGATAAGTGAATTATATAAAT

LysValValArgIleGluProLeuGlyValAlaProThrLysAlaLysArgArgValVal
ATAAAGTAGTAAGAATTGAACCCCTAGGAGTAGCACCCACCAAGGCAAAGAGAAGAGTGG
7300

GluArgGluLysArgAlaIleGlyLeuGlyAlaMetPheLeuGlyPheLeuGlyAlaAla
TGGAAAGAGAAAAAAGAGCAATAGGACTAGGAGCCATGTTCCTTGGGTTCTTGGGAGCAG

GlySerThrMetGlyAlaAlaSerLeuThrLeuThrValGlnAlaArgGlnLeuLeuSer
CAGGAAGCACGATGGGCGCAGCGTCACTAACGCTGACGGTACAGGCCAGACAGTTACTGT
7400

GlyIleValGlnGlnGlnAsnAsnLeuLeuArgAlaIleGluAlaGlnGlnHisLeuLeu
CTGGTATAGTGCAACAGCAAAACAATTTGCTGAGGGCTATAGAGGCGCAACAGCATCTGT

GlnLeuThrValTrpGlyIleLysGlnLeuGlnAlaArgValLeuAlaValGluArgTyr
TGCAACTCACGGTCTGGGGCATTAAACAGCTCCAGGCAAGAGTCCTGGCTGTGGAAAGAT
7500

LeuGlnAspGlnArgLeuLeuGlyMetTrpGlyCysSerGlyLysHisIleCysThrThr
ACCTACAGGATCAACGGCTCCTAGGAATGTGGGGTTGCTCTGGAAAACACATTTGCACCA

PheValProTrpAsnSerSerTrpSerAsnArgSerLeuAspAspIleTrpAsnAsnMet
CATTTGTGCCTTGGAACTCTAGTTGGAGTAATAGATCTCTAGATGACATTTGGAATAATA
7600

ThrTrpMetGlnTrpGluLysGluIleSerAsnTyrThrGlyIleIleTyrAsnLeuIle
TGACCTGGATGCAGTGGGAAAAAGAAATTAGCAATTACACAGGCATAATATACAACTTAA
7700

GluGluSerGlnIleGlnGlnGluLysAsnGluLysGluLeuLeuGluLeuAspLysTrp
TTGAAGAATCGCAAATCCAGCAAGAAAAGAATGAAAAGGAATTATTGGAATTGGACAAGT

AlaSerLeuTrpAsnTrpPheSerIleSerLysTrpLeuTrpTyrIleArgIlePheIle
GGGCAAGTTTGTGCAATTGGTTTAGCATATCAAAATGGCTCTGGTATATAAGAATATTCA
7800

IleValValGlyGlyLeuIleGlyLeuArgIleIlePheAlaValLeuSerLeuValAsn
TAATAGTAGTAGGAGGCTTAATAGGTTTAAGAATAATTTTTGCTGTGCTTTCTTTAGTAA

ArgValArgGlnGlyTyrSerProLeuSerLeuGlnThrLeuLeuProThrProArgGly
ATAGAGTTAGGCAGGGATACTCACCTCTGTCGTTGCAGACCCTCCTCCCAACACCGAGGG
7900

ProProAspArgProGluGlyIleGluGluGluGlyGlyGluGlnGlyArgGlyArgSer
GACCACCCGACAGGCCCGAAGGAATAGAAGAAGAAGGTGGAGAGCAAGGCAGAGGCAGAT
8000

IleArgLeuValAsnGlyPheSerAlaLeuIleTrpAspAspLeuArgAsnLeuCysLeu
CAATTCGATTGGTGAACGGATTCTCAGCACTTATCTGGGACGACCTGAGGAACCTGTCCC

PheSerTyrHisArgLeuArgAspLeuLeuLeuIleAlaThrArgIleValGluLeuLeu
TCTTCAGTTACCACCGCTTGAGAGACTTACTCTTAATTGCAACGAGGATTGTGGAACTTC
8100

GlyArgArgGlyTrpGluAlaLeuLysTyrLeuTrpAsnLeuLeuGlnTyrTrpGlyGln
TGGGACGCAGGGGGTGGGAAGCCCTCAAATATCTGTGGAATCTCCTGCAATATTGGGGTC
8200

FIG. 7I.

```
  GluLeuLysAsnSerAlaIleSerLeuLeuAsnThrThrAlaIleAlaValAlaGluCys
AGGAACTGAAGAATAGTGCTATTAGCTTGCTTAATACCACAGCAATAGCAGTAGCTGAAT

  ThrAspArgValIleGluIleGlyGlnArgPheGlyArgAlaIleLeuHisIleProArg
GCACAGATAGGGTTATAGAAATAGGACAAAGATTTGGTAGAGCTATTCTCCACATACCTA
              8300
                                                   F
                                  EW            MetGlyGlyLysTrpSerLys
  ArgIleArgGlnGlyPheGluArgAlaLeuLeu
GAAGAATTAGACAGGGCTTCGAAAGGGCTTTGCTATAACATGGGTGGCAAGTGGTCAAAA
                                                        8400
SerSerIleValGlyTrpProLysIleArgGluArgIleArgArgThrProProThrGlu
AGTAGCATAGTAGGATGGCCTAAGATTAGGAAAGAATAAGACGAACTCCCCCAACAGAA

ThrGlyValGlyAlaValSerGlnAspAlaValSerGlnAspLeuAspLysCysGlyAla
ACAGGAGTAGGAGCAGTATCTCAAGATGCAGTATCTCAAGATTTAGATAAATGTGGAGCA
                                        8500
AlaAlaSerSerSerProAlaAlaAsnAsnAlaSerCysGluProProGluGluGluGlu
GCCCGCAAGCAGCAGTCCAGCAGCTAATAATGCTAGTTGTGAACCACCAGAAGAAGAGGAG

GluValGlyPheProValArgProGlnValProLeuArgProMetThrTyrLysGlyAla
GAGGTAGGCTTTCCAGTCCGTCCTCAGGTACCTTTAAGACCAATGACTTATAAAGGAGCT
             8600                      U3
PheAspLeuSerHisPheLeuLysGluLysGlyGlyLeuAspGlyLeuValTrpSerPro
TTTGATCTCAGCCACTTTTTAAAAGAAAAGGGGGGACTGGATGGGTTAGTTTGGTCCCCA
                                                        8700
LysArgGlnGluIleLeuAspLeuTrpValTyrHisThrGlnGlyTyrPheProAspTrp
AAAAGACAAGAAATCCTTGATCTGTGGGTCTACCACACACAAGGCTACTTCCCTGATTGG

GlnAsnTyrThrProGlyProGlyIleArgPheProLeuThrPheGlyTrpCysPheLys
CAGAATTACACACCAGGGCCAGGGATTAGATTCCCACTGACCTTCGGATGGTGCTTTAAG
                                        8800
LeuValProMetSerProGluGluValGluGluAlaAsnGluGlyGluAsnAsnCysLeu
TTAGTACCAATGAGTCCAGAGGAAGTAGAGGAGGCCAATGAAGGAGAGAACAACTGTCTG

LeuHisProIleSerGlnHisGlyMetGluAspAlaGluArgGluValLeuLysTrpLys
TTACACCCTATTAGCCAACATGGAATGGAGGACGCAGAAAGAGAAGTGCTAAAATGGAAG
             8900
PheAspSerSerLeuAlaLeuArgHisArgAlaArgGluGlnHisProGluTyrTyrLys
TTTGACAGCAGCCTAGCACTAAGACACAGAGCCAGAGAACAACATCCGGAGTACTACAAA
  F                                                     9000
AspCys
GACTGCTGACACAGAAGTTGCTGACAGGGGACTTTCCGCTGGGGACTTTCCAGGGGAGGC

GTAACTTGGGCGGGACCGGGGAGTGGCTAACCCTCAGATGCTGCATATAAGCAGCTGCTT
          U3   R                        9100
TTCGCCTGTACTGGGTCTCTCTTGTTAGACCAGGTCGAGCCCGGGAGCTCTCTGGCTAGC

AAGGAACCCACTGCTTAAGCCTCAATAAAGCTTGCCTTGAGTGCCTCAA
             9200
```

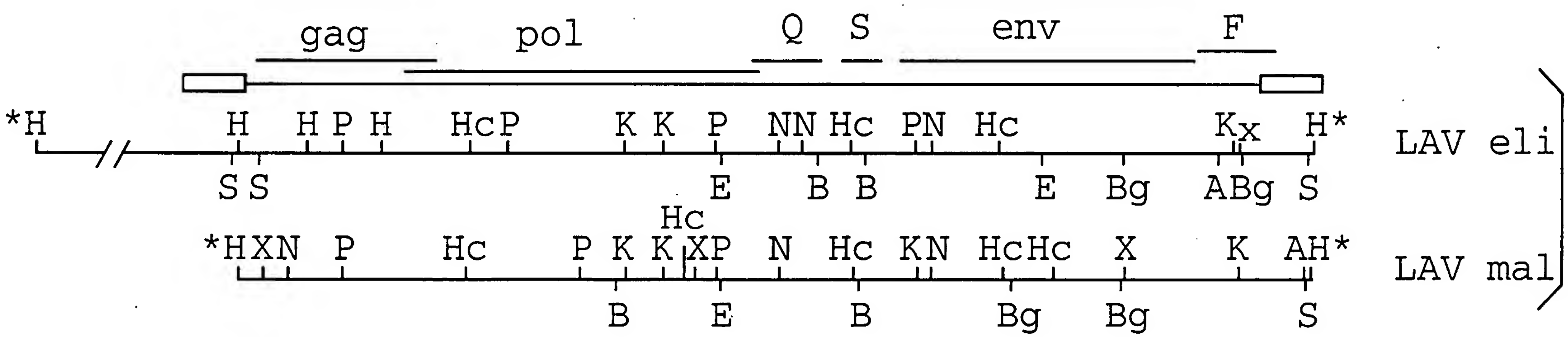

gag
pol
Q
S
env
F
LAV eli
LAV mal
*H
H H P H HcP K K P NN Hc PN Hc Kx H*
S S E B B E Bg ABg S
HXN P Hc P K K XP N Hc KN HcHc X K AH
Hc
B E B Bg Bg S

FIG. 1A

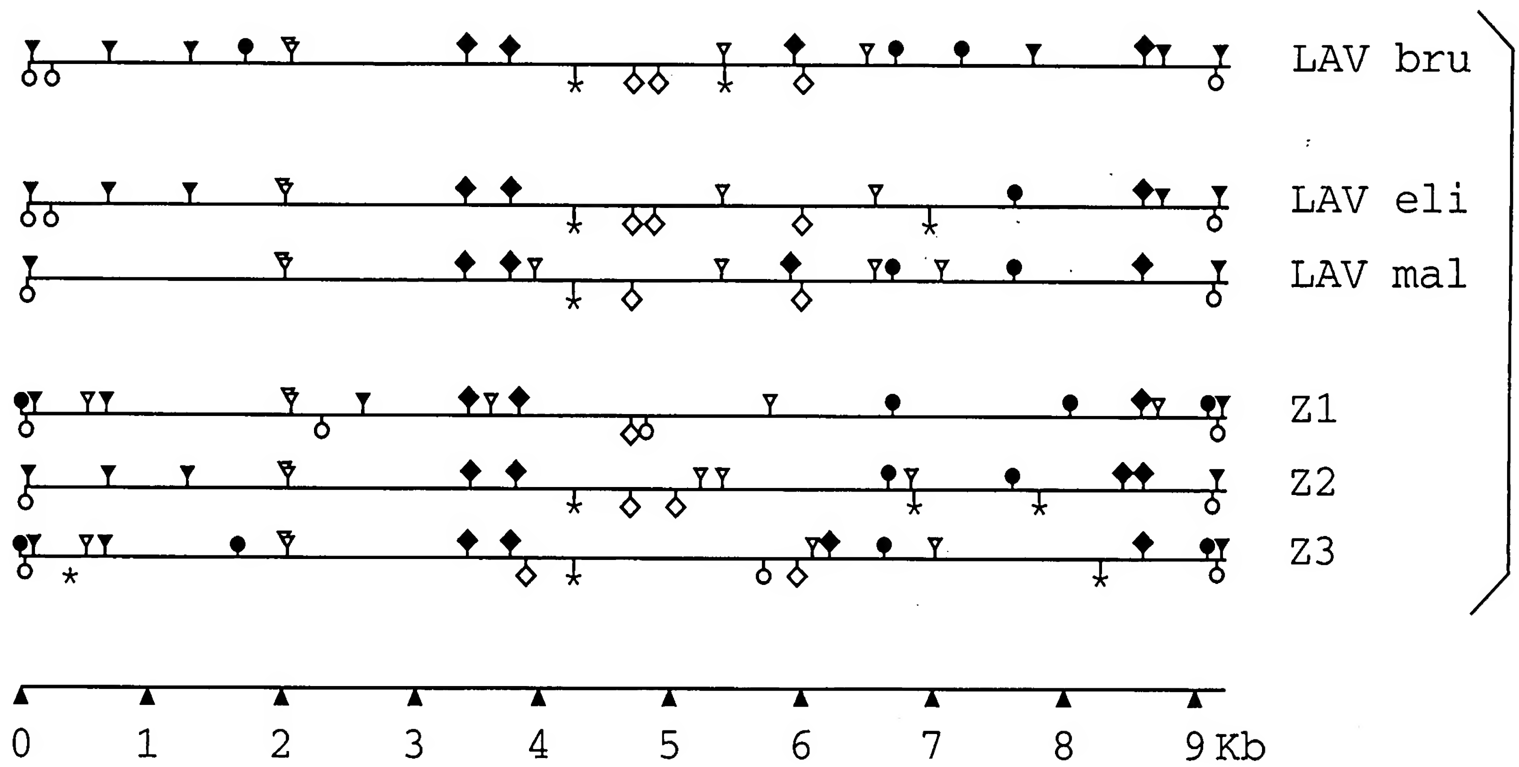


FIG. 1B

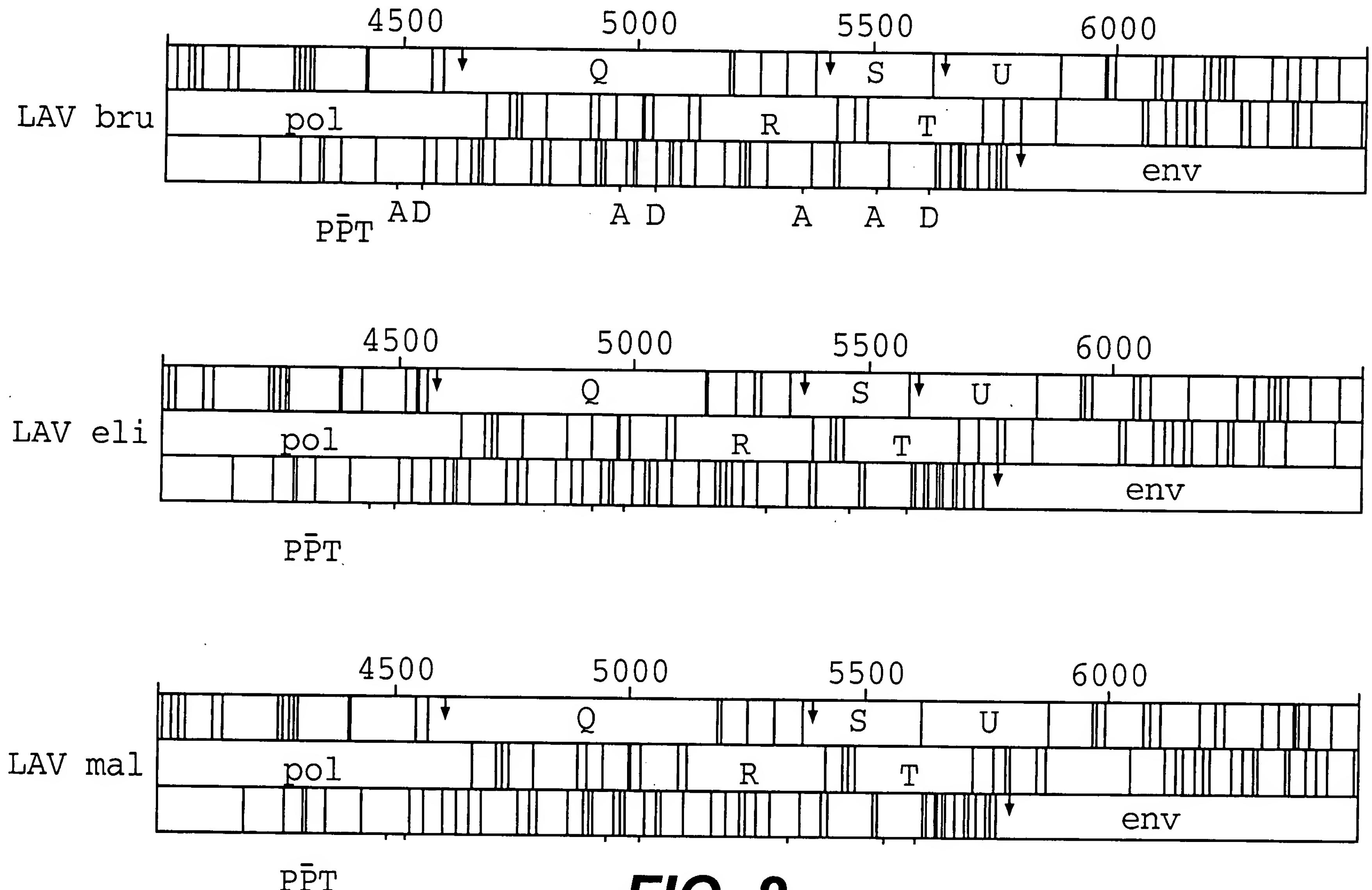

4500
5000
5500
6000
LAV bru
pol
Q
S
U
R
T
env
PP̄T
AD
A D
A
A
D
LAV eli
LAV mal

FIG. 2

GAG

```
                 10         20         30         40         50         60         70         80
LAV BRU  MGARASVLSG GELDRWEKIR LRPGGKKKYK LKHIVWASRE LERFAVNPGL LETSEGCRQI LGQLQPSLQT GSEELRSLYN
ARV 2                   K
LAV MAL              K  A               R    L            L       C    Q   ME   ST K      IK
LAV ELI              K  K               R               Y L            K   I     AI    T
                                                                       ↓p25
                 90        100        110        120        130        140        150        160
LAV BRU  TVATLYCVHQ RIEIKDTKEA LDKIEEEQNK SKKKAQQAAA ------DTGH SSQVSQNYPI VQNIQGQMVH QAISPRTLNA
ARV 2                 DV        E                    ----AAG  N               L
LAV MAL               DV            I     RQ T       AQQAAAA KN  S            A    I
LAV ELI           K G DV        E M                  ------   N N             L

                170        180        190        200        210        220        230        240
LAV BRU  WVKVVEEKAF SPEVIPMFSA LSCGATPQDL NTMLNTVGGH QAAMQMLKET INEEAAEWDK VHPVHAGPIA PGQMREPRGS
ARV 2
LAV MAL      I                             M   I             D        D             P
LAV ELI      I                                                             L

                250        260        270        280        290        300        310        320
LAV BRU  DIAGTTSTLQ EQIGWMTNNP PIPVGEIYKR WIILGLNKIV RMYSPTSILD IRQGPKEPFR DYVDRFYKTL RAEQASQEVK
ARV 2                                                                                        D
LAV MAL                    S        D                     V                      F         T
LAV ELI                A   S                 V            V                                  D
```

FIG. 3A-1

```
                 330        340        350        360        370        380   |p13    390        400
LAV BRU  NWMTETLLVQ NANPDCKTIL KALGPAATLE EMMTACQGVG GPGHKARVLA EAMSQVTNS- ATIMMQRGNF RNQRKIVKCF
ARV 2                                                                        P-  N               T
LAV MAL                              G                    S          A    T  A            KG - RI
LAV ELI                              Q                    S          A    V T A           KGP   I

                 410        420        430        440        450        460        470        480
LAV BRU  NCGKEGHIAR NCRAPRKKGC WKCGKEGHQM KDCTERQANF LGKIWPSYKG RPGNFLQSRP EPTAPPFLQS RPEPTAPPEE
ARV 2             K            R  R
LAV MAL         L                                           H                      ---- --------
LAV ELI           K            R       L                 R   H                     ---- --------A
                                                                                   ---- --------A

                 490        500        510
LAV BRU  SFRSGVETTT PSQKQEPIDK ELYPLTSLRS LFGNDPSSQ
ARV 2      F E K
LAV MAL    GF E IK-      QK         A  K       QL
LAV ELI    GF E I -      QK            K        L
```

FIG. 3A-2

```
CENTRAL REGION:  Q
                 10         20         30         40         50         60         70         80
LAV BRU  MENRWQVMIV WQVDRMRIRT WKSLVKHHMY VSGKARGWFY RHHYESPHPR ISSEVHIPLG DARLVITTYW GLHTGERDWH
ARV 2                                     I K  K           T    V            K               E
LAV MAL                         H           K  KN          R  K V               VR      Q   K
LAV ELI                     K               K  NR             K            E     K           E

                 90        100        110        120        130        140        150        160
LAV BRU  LGQGVSIEWR KKRYSTQVDP ELADQLIHLY YFDCFSDSAI RKALLGHIVS PRCEYQAGHN KVGSLQYLAL AALITPKKIK
ARV 2         A       K        G        H       E    KN I  YR                                 T
LAV MAL    H        Q      L   D                E     Q I          D                  T   A   TR
LAV ELI              R         G       M        E       I  D                          T   A  Q

                170        180        190
LAV BRU  PPLPSVTKLT EDRWNKPQKT KGHRGSHTMN GH
ARV 2          K
LAV MAL        R            Q
LAV ELI        R            Q  R
```

FIG. 3B-1

```
             R
              10         20         30         40         50         60         70         80
LAV BRU  MEQAPEDQGP QREPHNEWTL ELLEELKNEA VRHFPRIWLH GLGQHIYETY GDTWAGVEAI IRILQQLLFI HFRIGCRHSR
ARV 2                   Y          R          P     S   Y                                  Q
LAV MAL      A                     Q                S              E        S              Q
LAV ELI      A          Y   A      S                S              V                       Q

              90
LAV BRU  IGVTQQRRAR -NGASRS
ARV 2     II        R
LAV MAL   I R       -  S
LAV ELI   IIR       -  S

            S (tat)

              10         20         30         40         50         60         70
LAV BRU  MEPVDPRLEP WKHPGSQPKT ACTTCYCKKC CFHCQVCFTT KALGISYGRK KRRQRRRPPQ GSQTHQVSLS KQ
ARV 2         N          R    NN           YA  R  G                 A  D    A
LAV MAL   D    N    N    R  P NK        Y   M  I  G                     N A  DP P E
LAV ELI   D    N    N    R  P NK H      Y  P   LN G                G    G A   PIP
```

FIG. 3B-2

POL

```
                  10          20          30          40          50          60          70          80
LAV BRU   FFREDLAFLQ GKAREFSSEQ TRANSPTFSS EQTRANSPTR RELQVWGRDN NSLSEAGADR QGTVSFNFPQ ITLWQRPLVT
ARV 2                                  --- ---------          GE
LAV MAL       N   P         P          --- ---------S     R   G  -KT   T  E   I    S           V
LAV ELI       N   P     G L PK         --- ---------S     R      - P  KT  E                      A

                  90         100         110         120         130         140         150         160
LAV BRU   IKIGGQLKEA LLDTGADDTV LEEMSLPGRW KPKMIGGIGG FIKVRQYDQI LIEICGHKAI GTVLVGPTPV NIIGRNLLTQ
ARV 2      R                        N   K                        PV
LAV MAL   VRV                      IN   K                              K      I              M
LAV ELI                             N   K                        P     Q

                 170         180         190         200         210         220         230         240
LAV BRU   IGCTLNFPIS PIETVPVKLK PGMDGPKVKQ WPLTEEKIKA LVEICTEMEK EGKISKIGPE NPYNTPVFAI KKKDSTKWRK
ARV 2
LAV MAL                               R                T    KD       L
LAV ELI                                                T     D        R           I

                 250         260         270         280         290         300         310         320
LAV BRU   LVDFRELNKR TQDFWEVQLG IPHPAGLKKK KSVTVLDVGD AYFSVPLDED FRKYTAFTIP SINNETPGIR YQYNVLPQGW
ARV 2                                                       K
LAV MAL     N
LAV ELI                                                             S
```

FIG. 3C-1

```
                330        340        350        360        370        380        390        400
LAV BRU  KGSPAIFQSS MTKILEPFRK QNPDIVIYQY MDDLYVGSDL EIGQHRTKIE ELRQHLLRWG LTTPDKKHQK EPPFLWMGYE
ARV 2                                                                       F
LAV MAL                      T K  E                                 E   K   F
LAV ELI                           EM                             K  E       F R

                410        420        430        440        450        460        470        480
LAV BRU  LHPDKWTVQP IVLPEKDSWT VNDIQKLVGK LNWASQIYPG IKVRQLCKLL RGTKALTEVI PLTEEAELEL AENREILKEP
ARV 2                M                            A     K
LAV MAL              Q  D E                             K         A    DIV    A
LAV ELI           S  K    E         N  ER

                490        500        510        520        530        540        550        560
LAV BRU  VHGVYYDPSK DLIAEIQKQG QGQWTYQIYQ EPFKNLKTGK YARTRGAHTN DVKQLTEAVQ KITTESIVIW GKTPKFKLPI
ARV 2      E          V                                  M                   VS          I
LAV MAL                                     QY           IKS                  AQ             R
LAV ELI                         H                        M            A     R S         R    R
```

FIG. 3C-2

```
                 570        580        590        600        610        620        630        640
LAV BRU   QKETWETWWT EYWQATWIPE WEFVNTPPLV KLWYQLEKEP IVGAETFYVD GAASRETKLG KAGYVTNRGR QKVVTLTDTT
ARV 2           A  M                                                N             D        SIA
LAV MAL         A                                 T                 N    K        D        S  E
LAV ELI            A                                   I            N             D        P

                 650        660        670        680        690        700        710        720
LAV BRU   NQKTELQAIH LALQDSGLEV NIVTDSQYAL GIIQAQPDKS ESELVNQIIE QIIKKEKVYL AWVPAHKGIG GNEQVDKLVS
ARV 2                                                      S
LAV MAL                      S                            I          Q D     S
LAV ELI            N

                 730        740        750        760        770        780        790        800
LAV BRU   AGIRKVLFLD GIDKAQDEHE KYHSNWRAMA SDFNLPPVVA KEIVASCDKC QLKGEAMHGQ VDCSPGIWQL DCTHLEGKVI
ARV 2              N       E                                                                   I
LAV MAL   S                E                      I                                            I
LAV ELI Q                  E       N

                 810        820        830        840        850        860        870        880
LAV BRU   LVAVHVASGY IEAEVIPAET GQETAYFLLK LAGRWPVKTI HTDNGSNFTS TTVKAACWWA GIKQEFGIPY NPQSQGVVES
ARV 2
LAV MAL   I                            I           VV            AA         N
LAV ELI                                            VV            AA
```

FIG. 3D-1

```
                890        900        910        920        930        940        950        960
LAV BRU  MNKELKKIIG QVRDQAEHLK TAVQMAVFIH NFKRKGGIGG YSAGERIVDI IATDIQTKEL QKQITKIQNF RVYYRDSRDP
ARV 2      N                                                                                KK
LAV MAL                E                                    I M                             N
LAV ELI                                      RR             I                  I

                970        980        990       1000       1010
LAV BRU  LWKGPAKLLW KGEGAVVIQD NSDIKVVPRR KAKIIRDYGK QMAGDDCVAS RQDED
ARV 2
LAV MAL  I                                                    G G
LAV ELI  I                     K          V
```

FIG. 3D-2

ENV

```
                                        SP                                    OMP
                     10         20         30    ↓    40         50         60         70         80
LAV BRU  MRVK---EKY QHLWRWGWKW GTMLLGILMI CSATEKLWVT VYYGVPVWKE ATTTLFCASD AKAYDTEVHN VWATHACVPT
ARV 2     K  GTRRN             --- - L    M                                  R
LAV MAL     REIQRN   NW        --- -M     M  T   IA D                          S E       I
LAV ELI    ARGIERNC NW K       --- -I        T    ADN                          S E  A    I

                     90        100        110        120        130        140        150        160
LAV BRU  DPNPQEVVLV NVTENFNMWK NDMVEQMHED IISLWDQSLK PCVKLTPLCV SLKCTDL-CN ATNTNSSNTN SSSGEMMME-
ARV 2             C            N     Q                        T N    - K          --- ----NWKE I
LAV MAL         IE E     G     N                              T N  NVN T  V GTNACS  RTNA LK  I
LAV ELI         IA E           N                              T N S E--L RN GTMG NV TTEEKG----

                    170        180        190        200        210        220        230        240
LAV BRU  KGEIKNCSFN ISTSIRGKVQ KEYAFFYKLD IIPIDNDTTS -----YTLTS CNTSVITQAC PKVSFEPIPI HYCAPAGFAI
ARV 2                T    D I    N L RN   VV    AS T TNYTN R IN  R                       T
LAV MAL  -  V        TPVGSD R  -    T  N  LVQ  DSDN  ----S R IN                  T D
LAV ELI  ---M       VT VLKD K QV  L   R    V      SST -NSTN R IN    A

                    250        260        270        280        290        300        310        320
LAV BRU  LKCNKKTFNG TGPCTNVSTV QCTHGIRPVV STQLLLNGSL AEEEVVIRSA NFTDNAKTII VQLNQSVEIN CTRPNNNTRK
ARV 2                K                   I                       D    N            E  A
LAV MAL     D K       EI K            K                     IM   E  L   T N        ET T       G   R
LAV ELI    RD K                                              I    E  L N   N   AH   E  K T  A  YQ   Q
```

FIG. 3E-1

```
                330        340        350        360        370        380        390        400
LAV BRU  SIRIQRGPGR AFVTIGK-IG NMRQAHCNIS RAKWNATLKQ IASKLREQFG NNKT-IIFKQ SSGGDPEIVT HSFNCGGEFF
ARV 2      Y --        W T RI  DI K          Q  N  E   VK            - V N          M      R
LAV MAL  G HF--    Q  LY T I-V  DI R Y T N ETE DK  Q  V V  GSLL- -   K   NS         T      R
LAV ELI  RTP -- L Q SLY TKS-RS IIG            Q SK  Q  V R  GTLL- -   I K  P         T

                410        420        430        440        450        460        470        480
LAV BRU  YCNSTQLFNS TWFNSTWSTE CSNNTEGSDT ITLPCRIKQF INMWQEVGKA MYAPPISGQI RCSSNITGLL LTRDGGNN--
ARV 2       T     N   -----RLN RTEG K N   I        I                     C    S                T -V
LAV MAL     TSK       Q NGARL- -  S  STGS          I      KT             A V  N L      I       NSSD
LAV ELI     TSG       NI A NNI TES NSTNTN    Q     I  K VAGR-   I        ERN  L                 I --

                490        500        510        520        530        540        550        560
LAV BRU  NNGSEIFRPG GGDMRDNWRS ELYKYKVVKI EPLGVAPTKA KRRVVQREKR AVGI-GALFL GFLGAAGSTM GARSMTLTVQ
ARV 2    T DT V                       I      I                      V  M                   V L
LAV MAL   SDN TL             I        R                   E      I L-  M                   A L
LAV ELI   STN T                       Q          R        E      I L-  M                     V
```

FIG. 3E-2

```
                     570        580        590        600        610        620        630        640
LAV BRU  ARQLLSGIVQ QQNNLLRAIE AQQHLLQLTV WGIKQLQARI LAVERYLKDQ QLLGIWGCSG KLICTTAVPW NASWSNKSLE
ARV 2                                              W        R
LAV MAL                                            W        Q   R   M       H    F     S    R  D
LAV ELI      M                                                              H    N     S    R  N

                     650        660        670        680        690        700        710        720
LAV BRU  QIWNNMTWME WDREINNYTS LINSLIEESQ NQQEKNEQEL LELDKWASLW NWFNITNWLW YIKIFIMIVG GLVGLRIVFA
ARV 2    D  D     Q  E   D   N T YT L                           S
LAV MAL  D        Q  EK  S   G I YN       I      K                S SK      R   IV     I    I
LAV ELI  E  Q        E   D   G   Y        T      K                S  Q            I    I

                     730        740        750        760        770        780        790        800
LAV BRU  VLSIVNRVRQ GYSPLSFQTH LPTPRGP-DR PEGIEEEGGE RDRDRSIRLV NGSLALIWDD LRSLCLFSYH RLRDLLLIVT
ARV 2                       R   V    -    D               V    D F     E           R          AA
LAV MAL     L             L  L        P              QG G          FS          N                A
LAV ELI     L                L   A    -      T        G    V  L    FS                          I  AV

                     810        820        830        840        850        860        870
LAV BRU  RIVELLGRRG WEALKYWWNL LQYWSQELKN SAVSLLNATA IAVAEGTDRV IEVVQGACRA IRHIPRRIRQ GLERILL
ARV 2     T  I  K           S      I          W         T          A R Y    L  H          L
LAV MAL                   L        G        I    T        C       IG RFG    L          F  A
LAV ELI              DI   L            R    S  FD I               II R     VLN            S
```

FIG. 3F-1

F

```
                   10         20         30         40         50         60         70         80
LAV BRU  MGGKWSKSSV VGWPTVRERM R----RAEPA ADGVGAASR- ----DLEKUG AITSSNTAAT NAACAWLEAQ EE-EEVGFPV
ARV 2          R M G  SAI      RAEP            V  - ----                      D          -
LAV MAL          I     KI    I ---- TP T ET    V QD AVSQ  D C   AA  SP  N   S --- PP    E
LAV ELI          I     AI    I ---- TM         V  - ----                  S   D          SD

                   90        100        110        120        130        140        150        160
LAV BRU  TPQVPLRRHT YKAAVDLSHF LKEKGGLEGL IHSQRRQDIL DLWIYUTQGY FPDWQNYTPC PGVRYPLTFG WCYKLVPVEP
ARV 2    R                L  I             W     E                            I          F
LAV MAL  R              G F          D   VW PK   E      V                     I F        F    HS
LAV ELI  R              E L               W KK   E      V N   I               I           E    D

                  170        180        190        200        210
LAV BRU  DKVEEANKGE NTSLLHPVSL HGMDDPEREV LEWRFDSRLA FHHVARELHP EYFKNC
ARV 2    E      E    N     M     E A K    V     K      M        Y D
LAV MAL  EE     E    NC    I Q   E A     K K    S   LR R  Q     Y D
LAV ELI  QE   DTE    TN    ICQ   E    Q   K   N      E K  M    FY  -
```

FIG. 3F-2

A LAVbru vs.	GAG		POL		ENV					
					TOTAL		OMP		TMP	
HTLV-3 USA	512 0/0	0.8	1015 0/0	1.3	856 5/0	1.4	507 5/0	1.6	349 0/0	1.1
ARV-2 USA	502 12/2	3.4	1003 12/0	3.1	855 17/11	13.0	505 17/10	14.3	350 0/1	11.2
LAVeli ZAIRE	500 13/1	9.8	1002 13/0	5.5	853 22/14	20.7	504 22/14	25.3	349 0/0	13.8
LAVmal ZAIRE	505 14/7	12.0	1002 13/0	7.7	859 13/11	21.7	509 13/10	26.4	350 0/1	14.9
B LAVeli vs.										
LAVmal	505 1/6	10.8	1002 0/0	8.4	859 13/11	19.8	509 8/13	23.6	350 0/1	14.3

FIG. 4A

A LAVbru vs.	orf F		central region					
			orf Q		orf R		orf S	
HTLV-3 USA	206 0/0	1.5	192 0/0	0		nd	80 0/0	2.5
ARV-2 USA	210 0/4	12.6	192 0/0	10.0	97 0/1	9.4	81 0/1	15.0
LAVeli ZAIRE	206 1/1	19.4	192 0/0	10.4	96 0/0	11.5	80 0/0	27.5
LAVmal ZAIRE	209 2/5	27.0	192 0/0	12.6	96 0/0	10.4	80 0/0	23.8
B LAVeli vs.								
LAVmal	209 3/6	22.5	192 0/0	12.0	96 0/0	6.3	80 0/0	11.3

FIG. 4B

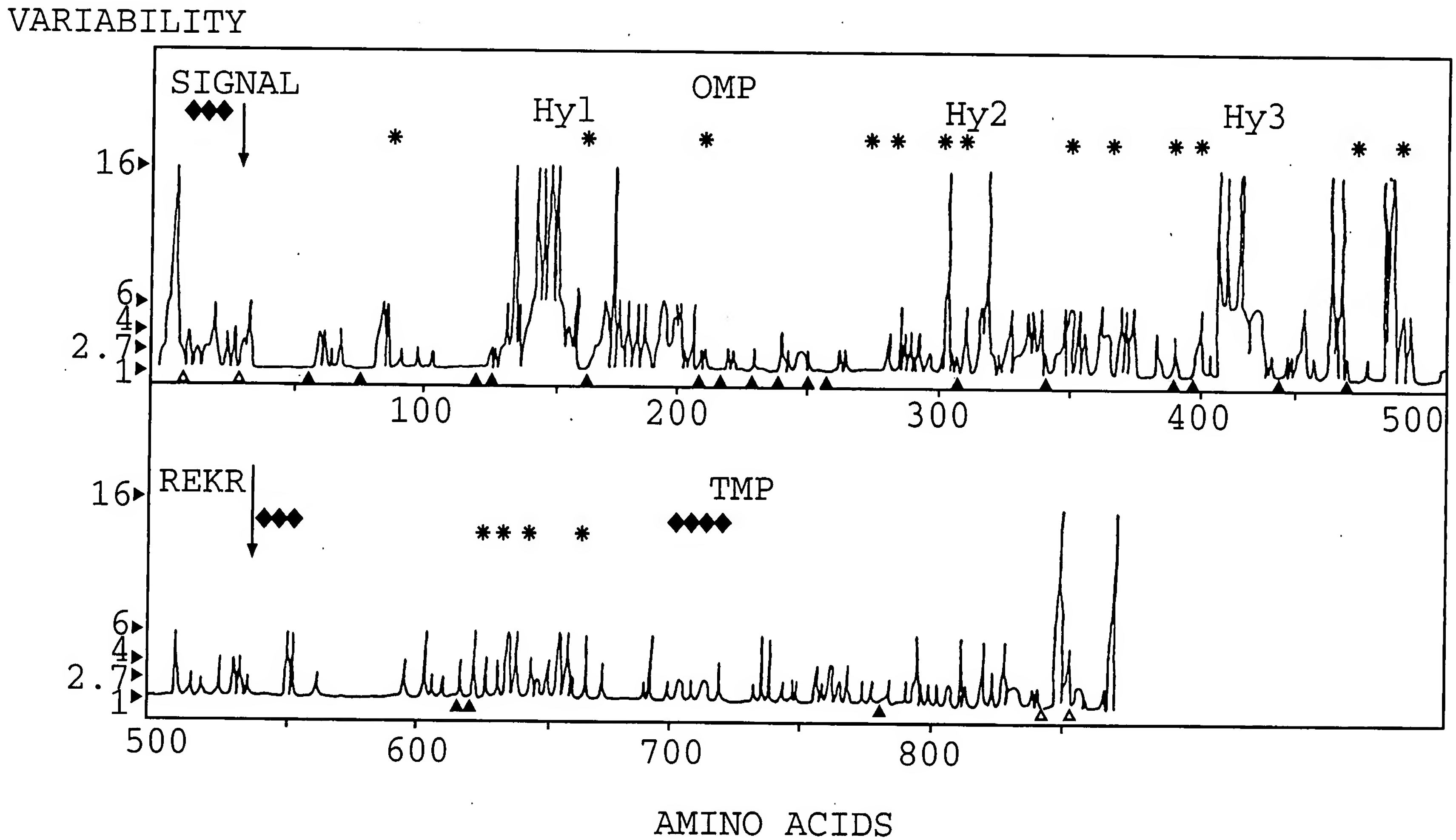

VARIABILITY
SIGNAL
Hy1
OMP
Hy2
Hy3
16
6
4
2.7
1
100
200
300
400
500
REKR
TMP
600
700
800
AMINO ACIDS

FIG. 5

GAG

a

```
                                 120

          K   A   Q   Q   A   A   A                           D   T
LAV.BRU  AAA GCA CAG CAA GCA GCA GCT  -   -   -   -   -       GAC ACA

          K   A   Q   Q   A   A   A   A   A   -   -   -   -   G   T
ARV 2    AAG GCA CAG CAA GCA GCA GCT GCA GCT                  GGC ACA

          K   T   Q   Q   A   A   A   A   Q   Q   A   A   A   A   T
LAV.MAL  AAG ACA CAG CAG GCA GCA GCT GCA GAG GAG GCA GCA GCT GCC ACA

          X   A   Q   Q   A   A   A                           D   T
LAV.ELI  AAG GCA CAG CAA GCA GCA GCT -   -   -   -   -   -     GAC ACA
```

FIG. 6A-1

b

```
LAV.BRU          460                                    470                                  480
G   N   F   L   Q   S   R   P   E   P   T   A   P   P   F   L   Q   S   R   P   E   P   T   A   P   P   E   E
GGG AAT TTT CTT CAG AGC AGA CCA GAG CCA ACA GCC CCA CCA TTT CTT CAG AGC AGA CCA GAG CCA ACA GCC CCA CCA GAA GAG

ARV 2

G   N   F   L   Q   S   R   P   E   P   T   A   P   P                                                   E   E
GGG AAT TTT CTT CAG AGC AGA CCA GAG CCA ACA GCC CCA CCA - - - - - - - - - - - - - - -                 GAA GAG

LAV.MAL

G   N   F   L   Q   S   R   P   E   P   T   A   P   P                                                   A   E
GGG AAT TTC CTT CAG AGC AGA CCA GAG CCA ACA GCC CCA CCA - - - - - - - - - - - - - - -                 GCA GAG

LAV.ELI

G   N   F   L   Q   S   R   P   E   P   T   A   P   P                                                   A   E
GGG AAC TTT CTC CAA AGC AGA CCA GAG CCA ACA GCC CCA CCA - - - - - - - - - - - - - - -                 GCA GAG
```

FIG. 6A-2

c

			20									30
	R	M	R					R	A	E	P	A
LAV.BRU	AGA	ATG	AGA	-	-	-	-	CGA	GCT	GAG	CCA	GCA
	R	M	R	R	A	E	P	R	A	E	P	A
ARV 2	AGA	ATG	AGA	CGA	GCT	GAG	CCA	CGA	GCT	GAG	CCA	GCA
	R	I	R					R	T	P	P	T
LAV.MAL	AGA	ATA	AGA	-	-	-	-	CGA	ACT	CCC	CCA	ACA
	R	I	R	-	-	-	-	R	T	P	P	T
LAV.ELI	AGA	ATA	AGA					AGA	ACT	AAT	CCA	GCA

d

						40						
	V	G	A	A	S	R						D
LAV.BRU	GTG	GGA	GCA	GCA	TCT	CGA	-	-	-	-	-	GAC
	V	G	A	V	A	R						D
ARV 2	GTG	GGA	GCA	GTA	TCT	CGA	-	-	-	-	-	GAC
	V	G	A	V	S	R	D	A	V	S	Q	D
LAV.MAL	GTA	GGA	GCA	GTA	TCT	CAA	GAT	GCA	GTA	TCT	CAA	GAT
	V	G	A	V	S	R						D
LAV.ELI	GTA	GGA	GCA	GTA	TCT	CGA	-	-	-	-	-	GAC

FIG. 6A-3

```
e                                          ENV
                                                20
           Q   H   L   W   R   W   G   W   K   W   G   T   M   L
LAV.BRU   CAG CAC TTG TGG ACA TGG GGC TGG AAA TGG GGC ACC ATG CTC

           Q   H   L   W   R   W   G                   T   L   L
ARV 2     CAG CAC TTG TGG AGA TGG GGC  -   -   -   -  ACC TTG CTC

           Q   N   W   W   R   W   G                   M   M   L
LAV.MAL   CAA AAC TGG TGG AGA TGG GGC  -   -   -   -  ATG ATG CTC

           Q   N   W   W   K   W   G                   T   M   L
LAV.ELI   CAA AAC TGG TGG AAA TCG GGC  -   -   -   -  ATC ATG CTC


f
LAV.BRU                             140                                       150
 L   K   C   T   D   L       G   N   A   T   N   T   N   S   S   N   T   N   S   S   S   G   E
TTA AAG TGC ACT GAT TTG  -  GGG AAT GCT ACT AAT ACC AAT AGT AGT AAT ACC AAT AGT AGT AGC GGG GAA
 M   M   M   E       K   G   E   I
ATG ATG ATG GAG  -  AAA GCA GAG ATA
ARG 2
 L   N   C   T   D   L       G   K   A   T   N   T   N   S   S                               M
TTA AAT TGC ACT GAT TTG  -  GGG AAG GCT ACT AAT ACC AAT AGT AGT  -   -   -   -   -   -   -  AAT
 W   K   E   E   I   K   G   E   I
TGG AAA GAA GAA ATA AAA GGA GAA ATA
```

FIG. 6B-1

LAV.MAL

```
 L   N   C   T   N   V   N   G   T   A   V   N   G   T   N   A   G   S   N   R   T   N   A   E
TTA AAC TGC ACT AAT GTG AAT GGG ACT GCT GTG AAT GGG ACT AAT GCT GGG AGT AAT AGG ACT AAT GCA GAA

 L   K   M   E   I       G   E   V
TTG AAA ATG GAA ATT  -  GGA GAA GTG
```

LAV.ELI

```
 L   N   C   S   D   E           L   R   N   N   G   T   M   G   N   N   V   T   T   E   E   K
TTA AAC TGT AGT GAT GAA  -   -  TTG AGG AAC AAT GGC ACT ATG GGG AAC AAT GTC ACT ACA GAG GAG AAA

 G                               M
GGA  -   -   -   -   -   -   -  ATG
```

FIG. 6B-2

```
g                                       200
              D   N   D   T   T   S                          Y   T   L
LAV.BRU      GAT AAT GAT ACT ACC AGC  -   -   -   -   -      TAT ACG TTG

              D   N   A   S   T   T   T   N   Y   T   N   Y   R   L
ARV 2        GAT AAT GCT AGT ACT ACT ACC AAC TAT ACC AAC TAT AGG TTG

              D   D   S   D   N   S   S                      Y   R   L
LAV.MAL      GAT GAT AGT GAT AAT AGT AGT  -   -   -   -      TAT AGG CTA

              D   N   D   S   S   T       N   S   T   N   Y   R   L
LAV.ELI      GAC AAT GAT AGT AGT ACC  -  AAT AGT ACC AAT TAT AGG TTA

h

LAV.BRU                         410                                         420                  430

 C   N   S   T   Q   L   F   N   S   T   W   F   N   S   T   W   S   T   E   G   S   N   N   T   E   G
TGT AAT TCA ACA CAA CTG TTT AAT AGT ACT TGG TTT AAT AGT ACT TGG AGT ACT GAA GGG TCA AAT AAC ACT GAA GGA

 S   D   T   I
AGT GAC ACA ATC

ARV 2

 C   N   T   T   Q   L   F   N   N   T   W                       R   L   N   H   T   K   G   T   K   G
TGT AAT ACA ACA CAA CTG TTT AAT AAT ACA TGG  -   -   -   -   -  AGG TTA AAT CAC ACT GAA GGA ACT AAA GGA

 N   D   T   I
AAT GAC ACA ATC
```

FIG. 6B-3

```
LAV.MAL

 C   N   T   S   K   L   F   N   S   T   W   Q   N   N   G   A   R   L           S   N   S   T   E   S
TGT AAT ACA TCA AAA CTG TTT AAT AGT ACA TGG CAG AAT AAT GGT GCA AGA CTA  -   -  AGT AAT AGC ACA GAG TCA

 T   G   S   I
ACT GGT AGT ATC

LAV.ELI

 C   N   T   S   G   L   F   N   S   T   W   N   I   S   A   W   N   N   I   T   E   S   N   N   S   T
TGT AAT ACA TCA GGA CTG TTT AAT AGT ACA TGG AAT ATT AGT GCA TGG AAT AAT ATT ACA GAG TCA AAT AAT AGC ACA

 N   T   N   I
AAC ACA AAC ATC
```

FIG. 6B-4

```
LAV.MAL
R
GGTCTCTCTTGTTAGACCAGGTCGAGCCCGGGAGCTCTCTGGCTAGCAAGGAACCCACTG
                                   R U5
CTTAAGCCTCAATAAAGCTTGCCTTGAGTGCCTCAAGCAGTGTGTGCCCATCTGTTGTGT
                                      100              U5
GACTCTGGTAACTAGAGATCCCTCAGACCACTCTAGACGGTGTAAAAATCTCTAGCAGTG

GCGCCCGAACAGGGACTTTAAAGTGAAAGTAACAGGGACTCGAAAGCGGAAGTTCCAGAG
                200
AAGTTCTCTCGACGCAGGACTCGGCTTGCTGAGGTGCACACAGCAAGAGGCGAGAGCGGC
                                                   GAG    300
                                                 MetGlyAlaArg
GACTGGTGAGTACGCCAATTTTTGACTAGCGGAGGCTAGAAGGAGAGAGATGGGTGCGAG

 AlaSerValLeuSerGlyGlyLysLeuAspAlaTrpGluLysIleArgLeuArgProGly
AGCGTCAGTATTAAGCGGGGGAAAATTAGATGCATGGGAGAAAATTCGGTTAAGGCCAGG
                                      400
 GlyLysLysLysTyrArgLeuLysHisLeuValTrpAlaSerArgGluLeuGluArgPhe
GGGAAAGAAAAAATATAGACTGAAACATTTAGTATGGGCAAGCAGGGAGCTGGAAAGATT

 AlaLeuAsnProGlyLeuLeuGluThrGlyGluGlyCysGlnGlnIleMetGluGlnLeu
CGCACTTAACCCTGGCCTTTTAGAAACAGGAGAAGGATGTCAACAAATAATGGAACAGCT
                500
 GlnSerThrLeuLysThrGlySerGluGluIleLysSerLeuTyrAsnThrValAlaThr
ACAATCAACTCTCAAGACAGGATCAGAAGAAATTAAATCATTATATAATACAGTAGCAAC
                                                          600
 LeuTyrCysValHisGlnArgIleAspValLysAspThrLysGluAlaLeuAspLysIle
CCTCTATTGTGTACATCAAAGGATAGATGTAAAAGACACCAAGGAAGCGCTAGATAAAAT

 GluGluIleGlnAsnLysSerArgGlnLysThrGlnGlnAlaAlaAlaAlaGlnGlnAla
AGAGGAAATACAAAATAAGAGCAGGCAAAAGACACAGCAGGCAGCAGCTGCACAGCAGGC
                                      700
 AlaAlaAlaThrLysAsnSerSerSerValSerGlnAsnTyrProIleValGlnAsnAla
AGCAGCTGCCACAAAAAACAGCAGCAGTGTCAGTCAAAATTACCCCATAGTGCAAAATGC

 GlnGlyGlnMetIleHisGlnAlaIleSerProArgThrLeuAsnAlaTrpValLysVal
ACAAGGGCAAATGATACATCAGGCCATATCACCTAGGACTTTGAATGCATGGGTGAAAGT
                800
 IleGluGluLysAlaPheSerProGluValIleProMetPheSerAlaLeuSerGluGly
AATAGAAGAAAAGGCTTTCAGCCCAGAAGTGATACCCATGTTCTCAGCATTATCAGAGGG
                                                          900
 AlaThrProGlnAspLeuAsnMetMetLeuAsnIleValGlyGlyHisGlnAlaAlaMet
GGCCACCCCACAAGATTTAAATATGATGCTGAACATAGTTGGAGGACACCAGGCAGCTAT

 GlnMetLeuLysAspThrIleAsnGluGluAlaAlaAspTrpAspArgValHisProVal
GCAAATGTTAAAAGATACCATCAATGAGGAAGCTGCAGACTGGGACAGGGTACATCCAGT
                                     1000
 HisAlaGlyProIleProProGlyGlnMetArgGluProArgGlySerAspIleAlaGly
ACATGCAGGGCCTATTCCCCCAGGCCAGATGAGAGAACCAAGAGGAAGTGACATAGCAGG
```

FIG. 7A

ThrThrSerThrLeuGlnGluGlnIleGlyTrpMetThrSerAsnProProIleProVal
AACTACTAGTACCCTTCAAGAACAAATAGGATGGATGACAAGCAACCCACCTATCCCAGT
1100
GlyAspIleTyrLysArgTrpIleIleLeuGlyLeuAsnLysIleValArgMetTyrSer
GGGAGACATCTATAAAAGATGGATAATCCTGGGATTAAATAAAATAGTAAGAATGTATAG
1200
ProValSerIleLeuAspIleArgGlnGlyProLysGluProPheArgAspTyrValAsp
CCCTGTCAGCATTTTGGACATAAGACAAGGGCCAAAGGAACCTTTTAGAGACTATGTAGA
ArgPhePheLysThrLeuArgAlaGluGlnAlaThrGlnGluValLysAsnTrpMetThr
TAGGTTCTTTAAAACTCTCAGAGCTGAGCAAGCTACACAGGAGGTAAAAAATTGGATGAC
1300
GluThrLeuLeuValGlnAsnAlaAsnProAspCysLysThrIleLeuLysAlaLeuGly
AGAAACCTTGCTGGTCCAAAATGCGAATCCAGACTGTAAGACCATTTTAAAAGCATTAGG
ProGlyAlaThrLeuGluGluMetMetThrAlaCysGlnGlyValGlyGlyProSerHis
ACCAGGGGCTACATTAGAAGAAATGATGACAGCATGCCAGGGAGTGGGAGGACCCAGTCA
1400
LysAlaArgValLeuAlaGluAlaMetSerGlnAlaThrAsnSerThrAlaAlaIleMet
TAAAGCAAGAGTTTTGGCTGAGGCAATGAGCCAAGCAACAAATTCAACTGCTGCCATAAT
1500
MetGlnArgGlyAsnPheLysGlyGlnLysArgIleLysCysPheAsnCysGlyLysGlu
GATGCAGAGAGGTAATTTTAAGGGCCAGAAAAGAATTAAGTGTTTCAACTGTGGCAAAGA
GlyHisLeuAlaArgAsnCysArgAlaProArgLysLysGlyCysTrpLysCysGlyLys
AGGACACCTAGCCAGAAATTGCAGGGCCCCTAGGAAAAAGGGCTGTTGGAAATGTGGGAA
1600 →POL
PhePheArgGluAsnLeu
GluGlyHisGlnMetLysAspCysThrGluArgGlnAlaAsnPheLeuGlyLysIleTrp
GGAAGGACACCAAATGAAAGACTGCACTGAGAGACAGGCTAATTTTTTAGGGAAAATTTG
AlaPheProGlnGlyLysAlaArgGluPheProSerGluGlnThrArgAlaAsnSerPro
ProSerHisLysGlyArgProGlyAsnPheLeuGlnSerArgProGluProThrAlaPro
GCCTTCCCACAAGGGAAGGCCAGGGAATTTCCTTCAGAGCAGACCAGAGCCAACAGCCCC
1700
ThrSerArgGluLeuArgValTrpGlyGlyAspLysThrLeuSerGluThrGlyAlaGlu
ProAlaGluSerPheGlyPheGlyGluGluIleLysProSerGlnLysGlnGluGlnLys
ACCAGCAGAGAGCTTCGGGTTTGGGGAGGAGATAAAACCCTCTCAGAAACAGGAGCAGAA
1800
ArgGlnGlyIleValSerPheSerPheProGlnIleThrLeuTrpGlnArgProValVal
AspLysGluLeuTyrProLeuAlaSerLeuLysSerLeuPheGlyAsnAspGlnLeuSer
AGACAAGGAATTGTATCCTTTAGCTTCCCTCAAATCACTCTTTGGCAACGACCAGTTGTC
GAG ←
ThrValArgValGlyGlyGlnLeuLysGluAlaLeuLeuAspThrGlyAlaAspAspThr
Gln
ACAGTAAGAGTAGGAGGACAGCTAAAAGAAGCTCTATTAGACACAGGAGCAGATGATACA
1900
ValLeuGluGluIleAsnLeuProGlyLysTrpLysProLysMetIleGlyGlyIleGly
GTATTAGAAGAAATAAATTTGCCAGGAAAATGGAAACCAAAAATGATAGGGGGAATTGGA
GlyPheIleLysValArgGlnTyrAspGlnIleLeuIleGluIleCysGlyLysLysAla
GGTTTTATCAAAGTAAGACAGTATGATCAAATACTTATAGAAATTTGTGGAAAAAAGGCT
2000

FIG. 7B

IleGlyThrIleLeuValGlyProThrProValAsnIleIleGlyArgAsnMetLeuThr
ATAGGTACAATATTGGTAGGACCTACACCTGTCAACATAATTGGACGAAATATGTTGACT
2100
GlnIleGlyCysThrLeuAsnPheProIleSerProIleGluThrValProValLysLeu
CAGATTGGTTGTACTTTAAATTTTCCAATTAGTCCTATTGAGACTGTACCAGTAAAATTA

LysProGlyMetAspGlyProArgValLysGlnTrpProLeuThrGluGluLysIleLys
AAGCCAGGGATGGATGGCCCAAGGGTTAAACAATGGCCATTGACAGAAGAAAAAATAAAA
2200
AlaLeuThrGluIleCysLysAspMetGluLysGluGlyLysIleLeuLysIleGlyPro
GCATTAACAGAAATTTGTAAAGATATGGAAAAGGAAGGAAAAATTTTAAAAATTGGGCCT

GluAsnProTyrAsnThrProValPheAlaIleLysLysLysAspSerThrLysTrpArg
GAAAATCCATACAATACTCCAGTATTTGCCATAAAGAAAAAAGACAGCACTAAATGGAGA
2300
LysLeuValAsnPheArgGluLeuAsnLysArgThrGlnAspPheTrpGluValGlnLeu
AAATTAGTGAATTTCAGAGAGCTTAATAAAAGAACTCAAGATTTTTGGGAAGTTCAATTA
2400
GlyIleProHisProAlaGlyLeuLysLysLysLysSerValThrValLeuAspValGly
GGAATACCACATCCTGCTGGGTTGAAAAAGAAAAAATCAGTCACAGTATTGGATGTGGGG

AspAlaTyrPheSerValProLeuAspGluAspPheArgLysTyrThrAlaPheThrIle
GATGCATATTTTTCAGTCCCTTTAGATGAAGATTTCAGGAAGTATACTGCATTCACTATA
2500
ProSerIleAsnAsnGluThrProGlyIleArgTyrGlnTyrAsnValLeuProGlnGly
CCCAGTATTAATAATGAGACACCAGGGATTAGATATCAGTACAATGTGCTACCACAGGGA

TrpLysGlySerProAlaIlePheGlnSerSerMetThrLysIleLeuGluProPheArg
TGGAAAGGATCACCAGCAATATTCCAGAGTAGCATGACAAAAATCTTAGAACCCTTT AGA
2600
ThrLysAsnProGluIleValIleTyrGlnTyrMetAspAspLeuTyrValGlySerAsp
ACAAAAAATCCAGAAATAGTCATATACCAATACATGGATGATTTGTATGTAGGGTCTGAT
2700
LeuGluIleGlyGlnHisArgThrLysIleGluGluLeuArgGluHisLeuLeuLysTrp
TTAGAAATAGGACAACATAGAACAAAAATAGAGGAACTAAGAGAACATCTATTGAAATGG

GlyPheThrThrProAspLysLysHisGlnLysGluProProPheLeuTrpMetGlyTyr
GGATTTACCACACCAGACAAAAAGCATCAGAAAGAACCCCCATTTCTTTGGATGGGGTAT
2800
GluLeuHisProAspLysTrpThrValGlnProIleGlnLeuProAspLysGluSerTrp
GAACTCCACCCTGACAAATGGACAGTGCAGCCTATACAACTGCCAGACAAGGAAAGCTGG

ThrValAsnAspIleGlnLysLeuValGlyLysLeuAsnTrpAlaSerGlnIleTyrPro
ACTGTCAATGATATACAGAAATTGGTGGGAAAACTAAATTGGGCAAGTCAGATTTATCCA
2900
GlyIleLysValLysGlnLeuCysLysLeuLeuArgGlyAlaLysAlaLeuThrAspIle
GGAATTAAAGTAAAGCAATTATGTAAACTCCTTAGGGGAGCAAAAGCACTAACAGACATA
3000
ValProLeuThrAlaGluAlaGluLeuGluLeuAlaGluAsnArgGluIleLeuLysGlu
GTACCATTAACTGCAGAGGCAGAATTAGAATTGGCAGAGAACAGGGAAATTCTAAAAGAA

FIG. 7C

ProValHisGlyValTyrTyrAspProSerLysAspLeuIleAlaGluIleGlnLysGln
CCAGTGCATGGGGTATATTATGACCCATCAAAAGACTTAATAGCAGAAATACAGAAGCAG
3100

GlyGlnGlyGlnTrpThrTyrGlnIleTyrGlnGluGlnTyrLysAsnLeuLysThrGly
GGGCAAGGTCAATGGACATATCAAATATACCAAGAGCAATATAAAAATCTGAAAACAGGG

LysTyrAlaArgIleLysSerAlaHisThrAsnAspValLysGlnLeuThrGluAlaVal
AAGTATGCAAGAATAAAGTCTGCCCACACTAATGATGTAAAACAATTAACAGAAGCAGTG
3200

GlnLysIleAlaGlnGluSerIleValIleTrpGlyLysThrProLysPheArgLeuPro
CAAAAGATAGCCCAAGAAAGCATAGTAATATGGGGAAAAACTCCTAAATTTAGACTACCC
3300

IleGlnLysGluThrTrpGluAlaTrpTrpThrGluTyrTrpGlnAlaThrTrpIlePro
ATACAAAAAGAAACATGGGAGGCATGGTGGACAGAATATTGGCAAGCCACCTGGATCCCT

GluTrpGluPheValAsnThrProProLeuValLysLeuTrpTyrGlnLeuGluThrGlu
GAATGGGAGTTTGTCAATACTCCTCCCCTAGTAAAACTATGGTACCAGTTAGAAACAGAA
3400

ProIleValGlyAlaGluThrPheTyrValAspGlyAlaAlaAsnArgGluThrLysLys
CCCATAGTAGGAGCAGAAACTTTCTATGTAGATGGGGCAGCTAATAGAGAAACTAAAAAG

GlyLysAlaGlyTyrValThrAspArgGlyArgGlnLysValValSerLeuThrGluThr
GGAAAAGCAGGATATGTTACTGACAGAGGAAGACAAAAGGTTGTCTCCTTAACTGAAACA
3500

ThrAsnGlnLysThrGluLeuGlnAlaIleHisLeuAlaLeuGlnAspSerGlySerGlu
ACAAATCAGAAGACTGAATTACAAGCAATCCACTTAGCTTTACAGGATTCAGGATCAGAA
3600

ValAsnIleValThrAspSerGlnTyrAlaLeuGlyIleIleGlnAlaGlnProAspLys
GTAAACATAGTAACAGACTCACAGTATGCATTAGGGATTATTCAAGCACAACCAGATAAA

SerGluSerGluIleValAsnGlnIleIleGluGlnLeuIleGlnLysAspLysValTyr
AGTGAATCAGAGATTGTTAATCAAATAATAGAGCAATTAATACAGAAGGACAAGGTCTAC
3700

LeuSerTrpValProAlaHisLysGlyIleGlyGlyAsnGluGlnValAspLysLeuVal
CTGTCATGGGTACCAGCACACAAAGGGATTGGAGGAAATGAACAAGTAGATAAATTAGTC

SerSerGlyIleArgLysValLeuPheLeuAspGlyIleAspLysAlaGlnGluGluHis
AGCAGTGGAATCAGAAAGGTACTATTTTTAGATGGGATAGATAAGGCTCAAGAAGAACAT
3800

GluLysTyrHisSerAsnTrpArgAlaMetAlaSerAspPheAsnLeuProProIleVal
GAAAAATATCACAGCAATTGGAGAGCAATGGCTAGTGACTTTAATCTACCACCTATAGTA
3900

AlaLysGluIleValAlaSerCysAspLysCysGlnLeuLysGlyGluAlaMetHisGly
GCGAAGGAAATAGTAGCCAGCTGTGATAAATGTCAACTAAAAGGGGAAGCCATGCATGGA

GlnValAspCysSerProGlyIleTrpGlnLeuAspCysThrHisLeuGluGlyLysIle
CAAGTAGACTGTAGTCCAGGGATATGGCAATTAGATTGCACACATCTAGAAGGAAAAATA
4000

IleIleValAlaValHisValAlaSerGlyTyrIleGluAlaGluValIleProAlaGlu
ATCATAGTAGCAGTCCATGTAGCCAGTGGATATATAGAAGCAGAAGTTATCCCAGCAGAA

ThrGlyGlnGluThrAlaTyrPheIleLeuLysLeuAlaGlyArgTrpProValLysVal
ACAGGACAGGAGACAGCATACTTTATACTAAAATTAGCAGGAAGATGGCCAGTAAAAGTA
4100

FIG. 7D

```
ValHisThrAspAsnGlySerAsnPheThrSerAlaAlaValLysAlaAlaCysTrpTrp
GTACACACAGACAATGGCAGCAATTTCACCAGTGCTGCAGTTAAAGCAGCCTGTTGGTGG
                                                        4200
AlaAsnIleLysGlnGluPheGlyIleProTyrAsnProGlnSerGlnGlyValValGlu
GCAAATATCAAACAGGAATTTGGAATTCCCTACAACCCCCAAAGTCAAGGAGTAGTGGAA

SerMetAsnLysGluLeuLysLysIleIleGlyGlnValArgGluGlnAlaGluHisLeu
TCTATGAATAAGGAATTAAAGAAAATCATAGGGCAGGTAAGAGAGCAAGCTGAACACCTT
                                      4300
LysThrAlaValGlnMetAlaValPheIleHisAsnPheLysArgLysGlyGlyIleGly
AAGACAGCAGTACAAATGGCAGTGTTCATTCACAATTTTAAAAGAAAAGGGGGGATTGGG

GlyTyrSerAlaGlyGluArgIleIleAspMetIleAlaThrAspIleGlnThrLysGlu
GGGTACAGTGCAGGGGAAAGAATAATAGACATGATAGCAACAGACATACAAACTAAAGAA
                    4400
LeuGlnLysGlnIleThrLysIleGlnAsnPheArgValTyrTyrArgAspAsnArgAsp
TTACAAAAACAAATTACAAAAATTCAAAATTTTCGGGTTTATTACAGGGACAACAGAGAC
                                                        4500
ProIleTrpLysGlyProAlaLysLeuLeuTrpLysGlyGluGlyAlaValValIleGln
CCAATTTGGAAAGGACCAGCAAAACTACTCTGGAAAGGTGAAGGGGCAGTAGTAATACAG
                                                      Q
AspAsnSerAspIleLysValValProArgArgLysAlaLysIleIleArgAspTyrGly
                                                      MetGlu
GACAATAGTGATATAAAGGTAGTACCAAGAAGAAAAGCAAAAATCATTAGGGATTATGGA
                                      4600    POL
LysGlnMetAlaGlyAspAspCysValAlaGlyGlyGlnAspGluAsp
 AsnArgTrpGlnValMetIleValTrpGlnValAspArgMetArgIleArgThrTrpHis
AAACAGATGGCAGGTGATGATTGTGTGGCAGGTGGACAGGATGAGGATTAGAACATGGCA

 SerLeuValLysHisHisMetTyrValSerLysLysAlaLysAsnTrpPheTyrArgHis
CAGTTTAGTAAAACATCATATGTATGTCTCAAAGAAAGCTAAAAATTGGTTTTATAGACA
        4700
 HisTyrGluSerArgHisProLysValSerSerGluValHisIleProLeuGlyAspAla
TCACTATGAAAGCAGGCATCCAAAAGTAAGTTCAGAAGTACACATCCCACTAGGGGATGC
                                                        4800
 ArgLeuValValArgThrTyrTrpGlyLeuGlnThrGlyGluLysAspTrpHisLeuGly
TAGATTAGTAGTAAGAACATATTGGGGTCTGCAAACAGGAGAAAAAGACTGGCACTTGGG

 HisGlyValSerIleGluTrpArgGlnLysArgTyrSerThrGlnLeuAspProAspLeu
TCATGGGGTCTCCATAGAATGGAGGCAGAAAAGATATAGCACACAACTAGATCCTGACCT
                                      4900
 AlaAspGlnLeuIleHisLeuTyrTyrPheAspCysPheSerGluSerAlaIleArgGln
AGCAGACCAACTGATTCATCTGTACTATTTTGATTGTTTTTCAGAATCTGCCATAAGACA

 AlaIleLeuGlyHisIleValSerProArgCysAspTyrGlnAlaGlyHisAsnLysVal
AGCCATATTAGGACATATAGTTAGTCCTAGGTGTGATTATCAAGCAGGACATAACAAGGT
                    5000
 GlySerLeuGlnTyrLeuAlaLeuThrAlaLeuIleAlaProLysLysThrArgProPro
AGGATCTTTACAGTATTTGGCACTAACAGCATTAATAGCACCAAAAAAGACAAGGCCACC
                                    R                   5100
                                    MetGluGlnAlaProAlaAspGlnGly
 LeuProSerValArgLysLeuThrGluAspArgTrpAsnLysProGlnGlnThrLysGly
TTTGCCTAGTGTTAGGAAGCTAACAGAAGATAGATGGAACAAGCCCCAGCAGACCAAGGG
```

FIG. 7E

```
                                            Q
ProGlnArgGluProHisAsnGluTrpThrLeuGluLeuLeuGluGluLeuLysGlnGlu
 HisArgGlySerHisThrMetAsnGlyHis
CCACAGAGGGAGCCACACAATGAATGGACATTAGAACTTTTAGAGGAGCTTAAGCAAGAA
                                                5200
AlaValArgHisPheProArgIleTrpLeuHisSerLeuGlyGlnHisIleTyrGluThr
GCTGTCAGACACTTTCCTAGGATATGGCTCCATAGTTTAGGACAACATATCTATGAAACT

TyrGlyAspThrTrpGluGlyValGluAlaIleIleArgSerLeuGlnGlnLeuLeuPhe
TATGGGGATACCTGGGAAGGAGTTGAAGCTATAATAAGAAGTCTGCAACAACTGCTGTTT
                    5300
IleHisPheArgIleGlyCysGlnHisSerArgIleGlyIleThrArgGlnArgArgAla
ATTCATTTCAGAATTGGGTGTCAACATAGCAGAATAGGCATTACTCGACAGAGAAGAGCA
     S          R                                       5400
ArgAsnGlySerSerArgSer
    MetAspProValAspProAsnLeuGluProTrpAsnHisProGlySerGlnProArg
AGAAATGGATCCAGTAGATCCTAACTTAGAGCCCTGGAACCATCCAGGGAGTCAGCCTAG

 ThrProCysAsnLysCysTyrCysLysLysCysCysTyrHisCysGlnMetCysPheIle
GACGCCTTGTAATAAGTGTTATTGTAAAAAGTGCTGCTATCATTGCCAAATGTGCTTCAT
                                                5500
 ThrLysGlyLeuGlyIleSerTyrGlyArgLysLysArgArgGlnArgArgArgProPro
AACGAAAGGCTTAGGCATCTCCTATGGCAGGAAGAAGCGGAGACAGCGACGAAGACCTCC
                                            S
 GlnGlyAsnGlnAlaHisGlnAspProLeuProGluGln
TCAGGGCAATCAGGCTCATCAAGATCCTCTACCAGAGCAGTAAGTAGTATATGTAATACA
                    5600
ACCTTTAGTGATATTAGCAATAGTAGCATTAGTAGTAACGCTAATAATAGCAATAGTTGT
                                                            5700
GTGGACCATAGTATTTATAGAAATTAGGAAAATAAGAAGACAAAGGAAAATAGACAGGTT
                                                ENV
                                                MetArgValArgGluIleGlnArg
GATTGATAGAATAAGAGAAAGAGCAGAAGATAGTGGCAATGAGAGTGAGGGAGATACAGA
                                                5800
  AsnTyrGlnAsnTrpTrpArgTrpGlyMetMetLeuLeuGlyMetLeuMetThrCysSer
GGAATTATCAAAACTGGTGGAGATGGGGCATGATGCTCCTTGGGATGTTGATGACCTGTA

  IleAlaGluAspLeuTrpValThrValTyrTyrGlyValProValTrpLysGluAlaThr
GTATTGCAGAAGATTTGTGGGTTACAGTTTATTATGGGGTACCTGTGTGGAAAGAAGCAA
                    5900
  ThrThrLeuPheCysAlaSerAspAlaLysSerTyrGluThrGluValHisAsnIleTrp
CCACTACTCTATTTTGTGCATCAGATGCTAAATCATATGAAACAGAAGTACATAACATCT
                                                            6000
  AlaThrHisAlaCysValProThrAspProAsnProGlnGluIleGluLeuGluAsnVal
GGGCTACACATGCCTGTGTACCCACGGACCCCAACCCACAAGAAATAGAACTGGAAAATG

  ThrGluGlyPheAsnMetTrpLysAsnAsnMetValGluGlnMetHisGluAspIleIle
TCACAGAAGGGTTTAACATGTGGAAAAATAACATGGTGGAGCAGATGCATGAGGATATAA
                                                6100
```

FIG. 7F

```
SerLeuTrpAspGlnSerLeuLysProCysValLysLeuThrProLeuCysValThrLeu
TCAGTTTATGGGATCAAAGCCTAAAACCATGTGTAAAGCTAACCCCACTCTGTGTCACTT

AsnCysThrAsnValAsnGlyThrAlaValAsnGlyThrAsnAlaGlySerAsnArgThr
TAAACTGCACTAATGTGAATGGGACTGCTGTGAATGGGACTAATGCTGGGAGTAATAGGA
              6200
AsnAlaGluLeuLysMetGluIleGlyGluValLysAsnCysSerPheAsnIleThrPro
CTAATGCAGAATTGAAAATGGAAATTGGAGAAGTGAAAAACTGCTCTTTCAATATAACCC
                                                          6300
ValGlySerAspLysArgGlnGluTyrAlaThrPheTyrAsnLeuAspLeuValGlnIle
CAGTAGGAAGTGATAAAAGGCAAGAATATGCAACTTTTTATAACCTTGATCTAGTACAAA

AspAspSerAspAsnSerSerTyrArgLeuIleAsnCysAsnThrSerValIleThrGln
TAGATGATAGTGATAATAGTAGTTATAGGCTAATAAATTGTAATACCTCAGTAATTACAC
                                        6400
AlaCysProLysValThrPheAspProIleProIleHisTyrCysAlaProAlaGlyPhe
AGGCTTGTCCAAAGGTAACCTTTGATCCAATTCCCATACATTATTGTGCCCCAGCTGGTT

AlaIleLeuLysCysAsnAspLysLysPheAsnGlyThrGluIleCysLysAsnValSer
TTGCAATTCTAAAGTGTAATGATAAGAAGTTCAATGGAACGGAAATATGTAAAAATGTCA
              6500
ThrValGlnCysThrHisGlyIleLysProValValSerThrGlnLeuLeuLeuAsnGly
GTACAGTACAATGTACACATGGAATTAAGCCAGTGGTGTCAACTCAACTGCTGTTAAATG
                                                          6600
SerLeuAlaGluGluGluIleMetIleArgSerGluAsnLeuThrAspAsnThrLysAsn
GCAGTCTAGCAGAAGAAGAGATAATGATTAGATCTGAAAATCTCACAGACAATACTAAAA

IleIleValGlnLeuAsnGluThrValThrIleAsnCysThrArgProGlyAsnAsnThr
ACATAATAGTACAGCTTAATGAAACTGTAACAATTAATTGTACAAGGCCTGGAAACAATA
                                        6700
ArgArgGlyIleHisPheGlyProGlyGlnAlaLeuTyrThrThrGlyIleValGlyAsp
CAAGAAGAGGGATACATTTCGGCCCAGGGCAAGCACTCTATACAACAGGGATAGTAGGAG

IleArgArgAlaTyrCysThrIleAsnGluThrGluTrpAspLysThrLeuGlnGlnVal
ATATAAGAAGAGCATATTGTACTATTAATGAAACAGAATGGGATAAAACTTTACAACAGG
              6800
AlaValLysLeuGlySerLeuLeuAsnLysThrLysIleIlePheAsnSerSerSerGly
TAGCTGTAAAACTAGGAAGCCTTCTTAACAAAACAAAAATAATTTTTAATTCATCCTCAG
                                                          6900
GlyAspProGluIleThrThrHisSerPheAsnCysArgGlyGluPhePheTyrCysAsn
GAGGGGACCCAGAAATTACAACACACAGTTTTAATTGTAGAGGGGAATTTTTCTACTGTA

ThrSerLysLeuPheAsnSerThrTrpGlnAsnAsnGlyAlaArgLeuSerAsnSerThr
ATACATCAAAACTGTTTAATAGTACATGGCAGAATAATGGTGCAAGACTAAGTAATAGCA
                                        7000
GluSerThrGlySerIleThrLeuProCysArgIleLysGlnIleIleAsnMetTrpGln
CAGAGTCAACTGGTAGTATCACACTCCCATGCAGAATAAAACAAATTATAAATATGTGGC

LysThrGlyLysAlaMetTyrAlaProProIleAlaGlyValIleAsnCysLeuSerAsn
AGAAAACAGGAAAAGCTATGTATGCCCCTCCCATCGCAGGAGTCATCAACTGTTTATCAA
              7100
IleThrGlyLeuIleLeuThrArgAspGlyGlyAsnSerSerAspAsnSerAspAsnGlu
ATATTACAGGGCTGATATTAACAAGAGATGGTGGAAATAGTAGTGACAATAGTGACAATG
                                                          7200
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FIG. 7G

ThrLeuArgProGlyGlyGlyAspMetArgAspAsnTrpIleSerGluLeuTyrLysTyr
AGACCTTAAGACCTGGAGGAGGAGATATGAGGGACAATTGGATAAGTGAATTATATAAAT

LysValValArgIleGluProLeuGlyValAlaProThrLysAlaLysArgArgValVal
ATAAAGTAGTAAGAATTGAACCCCTAGGAGTAGCACCCACCAAGGCAAAGAGAAGAGTGG
7300

GluArgGluLysArgAlaIleGlyLeuGlyAlaMetPheLeuGlyPheLeuGlyAlaAla
TGGAAAGAGAAAAAAGAGCAATAGGACTAGGAGCCATGTTCCTTGGGTTCTTGGGAGCAG

GlySerThrMetGlyAlaAlaSerLeuThrLeuThrValGlnAlaArgGlnLeuLeuSer
CAGGAAGCACGATGGGCGCAGCGTCACTAACGCTGACGGTACAGGCCAGACAGTTACTGT
7400

GlyIleValGlnGlnGlnAsnAsnLeuLeuArgAlaIleGluAlaGlnGlnHisLeuLeu
CTGGTATAGTGCAACAGCAAAACAATTTGCTGAGGGCTATAGAGGCGCAACAGCATCTGT
7500

GlnLeuThrValTrpGlyIleLysGlnLeuGlnAlaArgValLeuAlaValGluArgTyr
TGCAACTCACGGTCTGGGGCATTAAACAGCTCCAGGCAAGAGTCCTGGCTGTGGAAAGAT

LeuGlnAspGlnArgLeuLeuGlyMetTrpGlyCysSerGlyLysHisIleCysThrThr
ACCTACAGGATCAACGGCTCCTAGGAATGTGGGGTTGCTCTGGAAAACACATTTGCACCA
7600

PheValProTrpAsnSerSerTrpSerAsnArgSerLeuAspAspIleTrpAsnAsnMet
CATTTGTGCCTTGGAACTCTAGTTGGAGTAATAGATCTCTAGATGACATTTGGAATAATA

ThrTrpMetGlnTrpGluLysGluIleSerAsnTyrThrGlyIleIleTyrAsnLeuIle
TGACCTGGATGCAGTGGGAAAAAGAAATTAGCAATTACACAGGCATAATATACAACTTAA
7700

GluGluSerGlnIleGlnGlnGluLysAsnGluLysGluLeuLeuGluLeuAspLysTrp
TTGAAGAATCGCAAATCCAGCAAGAAAAGAATGAAAAGGAATTATTGGAATTGGACAAGT
7800

AlaSerLeuTrpAsnTrpPheSerIleSerLysTrpLeuTrpTyrIleArgIlePheIle
GGGCAAGTTTGTGGAATTGGTTTAGCATATCAAAATGGCTGTGGTATATAAGAATATTCA

IleValValGlyGlyLeuIleGlyLeuArgIleIlePheAlaValLeuSerLeuValAsn
TAATAGTAGTAGGAGGCTTAATAGGTTTAAGAATAATTTTTGCTGTGCTTTCTTTAGTAA
7900

ArgValArgGlnGlyTyrSerProLeuSerLeuGlnThrLeuLeuProThrProArgGly
ATAGAGTTAGGCAGGGATACTCACCTCTGTCGTTGCAGACCCTCCTCCCAACACCGAGGG

ProProAspArgProGluGlyIleGluGluGluGlyGlyGluGlnGlyArgGlyArgSer
GACCACCCGACAGGCCCGAAGGAATAGAAGAAGAAGGTGGAGAGCAAGGCAGAGGCAGAT
8000

IleArgLeuValAsnGlyPheSerAlaLeuIleTrpAspAspLeuArgAsnLeuCysLeu
CAATTCGATTGGTGAACGGATTCTCAGCACTTATCTGGGACGACCTGAGGAACCTGTGCC
8100

PheSerTyrHisArgLeuArgAspLeuLeuLeuIleAlaThrArgIleValGluLeuLeu
TCTTCAGTTACCACCGCTTGAGAGACTTACTCTTAATTGCAACGAGGATTGTGGAACTTC

GlyArgArgGlyTrpGluAlaLeuLysTyrLeuTrpAsnLeuLeuGlnTyrTrpGlyGln
TGGGACGCAGGGGGTGGGAAGCCCTCAAATATCTGTGGAATCTCCTGCAATATTGGGGTC
8200

FIG. 7H

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  GluLeuLysAsnSerAlaIleSerLeuLeuAsnThrThrAlaIleAlaValAlaGluCys
AGGAACTGAAGAATAGTGCTATTAGCTTGCTTAATACCACAGCAATAGCAGTAGCTGAAT

  ThrAspArgValIleGluIleGlyGlnArgPheGlyArgAlaIleLeuHisIleProArg
GCACAGATAGGGTTATAGAAATAGGACAAAGATTTGGTAGAGCTATTCTCCACATACCTA
                 8300                         F
                                 EW       MetGlyGlyLysTrpSerLys
  ArgIleArgGlnGlyPheGluArgAlaLeuLeu
GAAGAATTAGACAGGGCTTCGAAAGGGCTTTGCTATAACATGGGTGGCAAGTGGTCAAAA
                                                        8400
SerSerIleValGlyTrpProLysIleArgGluArgIleArgArgThrProProThrGlu
AGTAGCATAGTAGGATGGCCTAAGATTAGGAAAGAATAAGACGAACTCCCCCAACAGAA

ThrGlyValGlyAlaValSerGlnAspAlaValSerGlnAspLeuAspLysCysGlyAla
ACAGGAGTAGGAGCAGTATCTCAAGATGCAGTATCTCAAGATTTAGATAAATGTGGAGCA
                                    8500
AlaAlaSerSerSerProAlaAlaAsnAsnAlaSerCysGluProProGluGluGluGlu
GCCGCAAGCAGCAGTCCAGCAGCTAATAATGCTAGTTGTGAACCACCAGAAGAAGAGGAG

GluValGlyPheProValArgProGlnValProLeuArgProMetThrTyrLysGlyAla
GAGGTAGGCTTTCCAGTCCGTCCTCAGGTACCTTTAAGACCAATGACTTATAAAGGAGCT
                 8600                 U3
PheAspLeuSerHisPheLeuLysGluLysGlyGlyLeuAspGlyLeuValTrpSerPro
TTTGATCTCAGCCACTTTTTAAAAGAAAAGGGGGGACTGGATGGGTTAGTTTGGTCCCCA
                                                        8700
LysArgGlnGluIleLeuAspLeuTrpValTyrHisThrGlnGlyTyrPheProAspTrp
AAAAGACAAGAAATCCTTGATCTGTGGGTCTACCACACACAAGGCTACTTCCCTGATTGG

GlnAsnTyrThrProGlyProGlyIleArgPheProLeuThrPheGlyTrpCysPheLys
CAGAATTACACACCAGGGCCAGGGATTAGATTCCCACTGACCTTCGGATGGTGCTTTAAG
                                         8800
LeuValProMetSerProGluGluValGluGluAlaAsnGluGlyGluAsnAsnCysLeu
TTAGTACCAATGAGTCCAGAGGAAGTAGAGGAGGCCAATGAAGGAGAGAACAACTGTCTG

LeuHisProIleSerGlnHisGlyMetGluAspAlaGluArgGluValLeuLysTrpLys
TTACACCCTATTAGCCAACATGGAATGGAGGACGCAGAAAGAGAAGTGCTAAAATGGAAG
                 8900
PheAspSerSerLeuAlaLeuArgHisArgAlaArgGluGlnHisProGluTyrTyrLys
TTTGACAGCAGCCTAGCACTAAGACACAGAGCCAGAGAACAACATCCGGAGTACTACAAA
  F                                                     9000
AspCys
GACTGCTGACACAGAAGTTGCTGACAGGGGACTTTCCGCTGGGGACTTTCCAGGGGAGGC

GTAACTTGGGCGGGACCGGGGAGTGGCTAACCCTCAGATGCTGCATATAAGCAGCTGCTT
       U3  R                        9100
TTCGCCTGTACTGGGTCTCTCTTGTTAGACCAGGTCGAGCCCGGGAGCTCTCTGGCTAGC

AAGGAACCCACTGCTTAAGCCTCAATAAAGCTTGCCTTGAGTGCCTCAA
                 9200
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FIG. 7I